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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 90.8333 Seconds
(without alignments)
464.112 Million cell updates/sec

Title: US-09-674-857-1
Perfect score: 581
Sequence: 1 APPVAGPSVLPFPKPKDYL.....CKVSNKGLPSSIBKTIISKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	109	3	AAY54996 Mutated C
2	567	97.6	449	6	AEE37576 Human FD1
3	565	97.2	462	2	AAW14933 2A2 (Chim
4	565	97.2	462	2	AAW14934 2A2 (Chim
5	565	97.2	463	2	AAW14939 3F4 (Chim
6	565	97.2	463	2	AAW14940 3F4 (Chim
7	565	97.2	472	5	ABP51695 SGL.1-TPO
8	565	97.2	472	8	ADQ16647 Immunoglo
9	562	96.7	326	8	ADF77155 Anti-VAP-
10	562	96.7	447	8	ADQ17121 Humanised
11	562	96.7	462	8	ADF77154 Chimeric
12	559.5	96.3	110	3	AAY54998 Mutated C
13	559	96.2	436	7	ADM33853 Human HuE
14	559	96.2	436	8	ADR48984 HuBPO-L-F
15	559	96.2	448	7	ADM33376 Human GCS
16	554	95.4	109	2	AAR41709 Undefined
17	554	95.4	109	3	AAY54997 Mutated C
18	554	95.4	217	3	ABO7476 Amino aci
19	554	95.4	217	4	ABF76423 Human IGG
20	554	95.4	217	4	AAB67203 Human IGG
21	554	95.4	217	5	AAG78434 Native se
22	554	95.4	217	6	ABR42440 Human IGG
23	554	95.4	217	8	ADH75378 Human IGG
24	554	95.4	228	5	ABG31095 Human mat
25	554	95.4	228	8	ADR48993 Human IGG

26	554	95.4	310	8	ADS84436 Human ant
27	554	95.4	310	8	ADR68578 Human ant
28	554	95.4	326	4	AAE02643 Human imm
29	554	95.4	326	5	AAM47857 Human Ig-
30	554	95.4	326	5	ABG30462 Human ant
31	554	95.4	326	5	ABG77148 Anti-IgF-
32	554	95.4	326	6	AAE32916 Human imm
33	554	95.4	326	6	AAE32628 Human imm
34	554	95.4	326	6	AAO30894 Human imm
35	554	95.4	326	7	ADE97353 Human IGG
36	554	95.4	326	7	ADF75002 Human Ig
37	554	95.4	326	8	ADM41541 Anti-inte
38	554	95.4	326	8	ADQ95469 Human IGG
39	554	95.4	326	8	ADR28562 Human ant
40	554	95.4	381	2	AAY06895 Human IL-
41	554	95.4	432	2	AAR26782 CD4-gamma
42	554	95.4	432	2	AAR46678 CD4-gamma
43	554	95.4	432	3	AAY85079 Human CD4
44	554	95.4	432	4	AAB67322 CD4-gamma
45	554	95.4	432	4	AAB80883 Human CD4

ALIGNMENTS

RESULT 1
AAY54996
ID AAY54996 standard; protein; 109 AA.

XX AC AAY54996;
XX DT 17-FEB-2000 (first entry)
XX DE Mutated CH2 sequence G1deltaab.

XX KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIB;
XX KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
XX KW B cell activation; mast cell degeneration; phagocytosis; vasculitis;
XX KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
XX KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
XX KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
XX KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
XX KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
XX KW sickle cell anaemia; coronary artery occlusion.

XX OS Synthetic.

XX PN WO958572-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001441.

XX PR 08-MAY-1998; 98GB-00009951.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PI Armour KL, Clark MR, Williamson LM;

XX PS WPI; 2000-039075/03.

XX CC Immunoglobulin-derived binding molecules that do not activate complement
or trigger cytotoxic activities and maintaining desirable immunoglobulin
properties.

XX PS Claim 12; Fig 17; 81pp; English.

XX CC This sequence represents the mutated CH2 molecule G1deltaab, and is a
binding molecule of the invention. The recombinant binding molecule is
capable of binding a target molecule without triggering complement
dependent lysis, or the cell-mediated destruction of the target
comprises: (a) a binding domain capable of binding a target molecule; and
(b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcγγmαRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of graft-vs-
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC foetal/neonatal alloimmune thrombocytopenia and arthritis), alloimmunity (e.g.
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcγγmαRIIb and desirable
 CC IgG properties have been retained. The polypeptides do not contain non-
 CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)
 XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 581; DB 3; Length 109;
 Best Local Similarity 100.0%; Pred. No. 7.5e-52;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 |||||
 DB 1 APPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 |||||
 QY 61 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTSKAK 109
 |||||
 DB 61 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTSKAK 109
 |||||

RESULT 2
 AAE37576
 ID AAE37576 standard; protein; 449 AA.

XX AAE37576;
 XX
 XX 27-AUG-2003 (first entry)
 DT
 XX Human FDI2-Ig alphatp fusion protein variant.
 DE
 XX Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;
 KW human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; DI;
 KW D2; alpha tailpiece; alphatp; fusion protein; mutein; variant; mutant.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 218 /note= "Wild type Glu substituted with Pro"
 FT Misc-difference 219 /note= "Wild type Leu substituted with Val"
 FT Misc-difference 221 /note= "Wild type Gly substituted with Ala"
 XX
 XX WO2003040311-A2.

PN
 XX 15-MAY-2003.
 PD
 XX 24-OCT-2002; 2002WO-US034393.
 PF
 XX 25-OCT-2001; 2001US-0346231P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Arthos J, Cicala C, Fauci AS;
 XX
 XX WPI; 2003-441545/41.
 DR N-PSDB; ACC82877.

XX New CD4 polypeptide ligated at its C-terminus with a portion of an
 PT immunoglobulin, useful for preparing a composition for treating or
 PT preventing HIV-1 infection.
 XX
 PS Example 11; Page 67; 100pp; English.

XX The invention relates to a CD4 (cluster of differentiation factor 4)
 CC polypeptide ligated at its C-terminus with a portion of an immunoglobulin
 CC (Ig) comprising a hinge region and a constant domain of a mammalian Ig
 CC heavy chain. The polypeptide comprises a tailpiece from the C-terminus of
 CC the heavy chain of an IGA or IGM antibody. Polypeptides of the invention
 CC are useful for preparing a composition for treating or preventing human
 CC immunodeficiency virus (HIV)-1 infection. The invention is useful in gene
 CC therapy and also in the preparation of vaccines. The present sequence is
 CC a fusion protein variant (G218P/L219V/220delA/G221A) which comprises a
 CC human IGA alpha tailpiece (alphatp), a human IGH2 constant region
 CC comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain.
 CC This variant protein is also referred to as mutant F
 XX
 SQ Sequence 449 AA;

Query Match 97.6%; Score 567; DB 6; Length 449;
 Best Local Similarity 97.2%; Pred. No. 1.2e-49;
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 |||||
 DB 216 APPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 275
 |||||
 QY 61 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTSKAK 109
 |||||
 DB 276 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTSKAK 324
 |||||

RESULT 3
 AAW14933
 ID AAW14933 standard; protein; 462 AA.

XX AAW14933;
 XX
 XX 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX
 XX 2A2 (Chimeric) human G2/G4 chimeric antibody.
 DE
 XX Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX WO9711971-A1.
 PN
 XX 03-APR-1997.
 PD
 XX 27-SEP-1996; 96WO-US015575.
 PF
 XX 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX
 XX (ALEX-) ALEXION PHARM INC.
 PA
 XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;
 PI
 XX WPI; 1997-212855/19.
 DR N-PSDB; AAT62931.
 XX
 XX Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.

XX Disclosure; Page 42-44; 105pp; English.

XX A chimeric antibody (AAW14933) comprises the C1 and hinge regions of

CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a

CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)

CC monoclonal antibody (MAB) 2A2 heavy chain variable region sequence (see

CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is

CC useful for diagnosing human rejection of porcine xenotransplants and for

CC improving xenotransplantation of porcine cells, tissues and organs into

CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 462 AA;

Query Match 97.2%; Score 565; DB 2; Length 462;

Best Local Similarity 97.2%; Pred. No. 1.9e-49;

Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

DB 247 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 306

QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109

DB 307 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 355

RESULT 4

AAW14934

ID AAW14934 standard; protein; 462 AA.

XX AC AAW14934;

XX DT 17-OCT-2003 (revised)

DT 16-JUN-1997 (first entry)

XX DE 2A2 (Chimeric) human G2/G4 chimeric antibody.

XX XE Xenotransplantation; graft rejection; cell interaction; pig;

KW vascular cell adhesion molecule; VCAM; monoclonal antibody;

KW chimeric antibody; diagnosis.

XX OS Homo; sapiens.

OS Mus sp.

OS Chimeric.

XX WO9711971-A1.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.

XX 26-SEP-1996; 96US-00004489.

XX (ALEX-) ALEXION PHARM INC.

XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;

PI WPI; 1997-212855/19.

DR N-PSDB; AAT62932.

XX Antibodies binding to porcine but not human cell interaction proteins -

PT useful to treat and assay for rejection of xenografted porcine organs,

PT tissues or cells.

XX Disclosure; Page 44-47; 105pp; English.

XX A chimeric antibody (AAW14934) comprises the C1 and hinge regions of

CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a

CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)

CC monoclonal antibody (MAB) 2A2 heavy chain variable region sequence (see

CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is

CC useful for diagnosing human rejection of porcine xenotransplants and for

CC improving xenotransplantation of porcine cells, tissues and organs into

CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 463 AA;

Query Match 97.2%; Score 565; DB 2; Length 463;

Best Local Similarity 97.2%; Pred. No. 1.9e-49;

Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

DB 247 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 306

QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109

DB 307 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 355

RESULT 5

AAW14939

ID AAW14939 standard; protein; 463 AA.

XX AC AAW14939;

XX DT 17-OCT-2003 (revised)

DT 16-JUN-1997 (first entry)

XX DE 3F4 (Chimeric) human G2/G4 chimeric antibody.

XX XE Xenotransplantation; graft rejection; cell interaction; pig;

KW vascular cell adhesion molecule; VCAM; monoclonal antibody;

KW chimeric antibody; diagnosis.

XX OS Homo; sapiens.

OS Mus sp.

OS Chimeric.

XX WO9711971-A1.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.

XX 26-SEP-1996; 96US-00004489.

XX (ALEX-) ALEXION PHARM INC.

XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;

PI WPI; 1997-212855/19.

DR N-PSDB; AAT62936.

XX Antibodies binding to porcine but not human cell interaction proteins -

PT useful to treat and assay for rejection of xenografted porcine organs,

PT tissues or cells.

XX Disclosure; Page 56-57; 105pp; English.

XX A chimeric antibody (AAW14939) comprises the C1 and hinge regions of

CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a

CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)

CC monoclonal antibody (MAB) 3F4 heavy chain variable region sequence (see

CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is

CC useful for diagnosing human rejection of porcine xenotransplants and for

CC improving xenotransplantation of porcine cells, tissues and organs into

CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 463 AA;

Query Match 97.2%; Score 565; DB 2; Length 463;

Best Local Similarity 97.2%; Pred. No. 1.9e-49;

Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

DB 247 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 306

QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109

DB 307 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 355

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316
 QY 61 REEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109
 Db 317 REEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 365

RESULT 8

ADQ16647
 ID ADQ16647 standard; protein; 472 AA.

XX AC ADQ16647;

XX DT 09-SEP-2004 (first entry)

XX DE Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67.

XX KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.

XX OS Synthetic.

XX PN WO2004050017-A2.

XX PD 17-JUN-2004.

XX PF 17-NOV-2003; 2003WO-US036894.

XX PR 02-DEC-2002; 2002US-00307724.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Frederickson S, Renshaw M;

XX DR WPI; 2004-460973/43.

XX DR N-PSDB; ADQ16648.

XX PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.

XX PS Example 4; SEQ ID NO 67; 107pp; English.

XX CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents an immunoglobulin antibody heavy chain of
 CC the invention.

XX SQ Sequence 472 AA;

Query Match 97.2%; Score 565; DB 8; Length 472;
 Best Local Similarity 97.2%; Pred. No. 2e-49;
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316

QY 61 REEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109

Db 317 REEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 365

RESULT 9

ADF77155
 ID ADF77155 standard; protein; 326 AA.

XX AC ADF77155;

XX DT 26-FEB-2004 (first entry)

XX DE Anti-VAP-1 monoclonal antibody H chain constant region.

XX KW complementarity determining region; CDR; mouse;
 KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
 KW chimeric; inflammatory disorder; rheumatoid arthritis;
 KW inflammatory bowel disease; autoimmune disease; psoriasis;
 KW immunoscintigraphic imaging.

XX OS Homo sapiens.

XX PN WO2003093319-A1.

XX PD 13-NOV-2003.

XX PF 28-APR-2003; 2003WO-FI000330.

XX PR 29-APR-2002; 2002FI-00000807.

XX PA (BIOT-) BIOTIE THERAPIES CORP.

XX PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;

XX DR WPI; 2004-022642/02.

XX PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
 PT encoding nucleic acid molecules, useful for diagnosing and treating
 PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.

XX PS Claim 18; SEQ ID NO 16; 56pp; English.

XX CC This sequence represents the constant region of a human anti-Vascular
 CC Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be
 CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The
 CC nucleic acid molecules, polypeptides or antibodies are useful in treating
 CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,
 CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
 CC chimeric VAP-1 antibody is further used for in vitro and in vivo
 CC diagnostic applications, including in vivo immunoscintigraphic imaging of
 CC inflammation sites. The chimeric Mab's of the invention have improved
 CC kinetic properties compared to the corresponding murine antibodies.

XX SQ Sequence 326 AA;

Query Match 96.7%; Score 562; DB 8; Length 326;
 Best Local Similarity 95.4%; Pred. No. 2.6e-49;
 Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 111 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170

QY 61 REEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109

Db 171 REEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 219

RESULT 10

ADQ17121
 ID ADQ17121 standard; protein; 447 AA.

XX AC ADQ17121;

XX DT 07-OCT-2004 (first entry)

XX DE Humanised anti-NGF antibody E3 heavy chain full-length protein.


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Query Match      96.7%; Score 562; DB 8; Length 462;
Best Local Similarity 95.4%; Pred. No. 4e-49;
Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cc 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Cc 247 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 306
Cc 61 REEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Cc 307 REEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 355

RESULT 12
AAI54998
ID AAY54998 standard; protein; 110 AA.
XX AC AAY54998;
XX DT 17-FEB-2000 (first entry)
XX DE Mutated CH2 sequence Gidelataac.
XX KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
XX KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
XX KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
XX KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
XX KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
XX KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
XX KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
XX KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
XX KW sickle cell anaemia; coronary artery occlusion.
XX OS Synthetic.
XX PN WO9958572-A1.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99WO-GB001441.
XX PR 08-MAY-1998; 98GB-00009951.
XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX PI Armour KL, Clark MR, Williamson LM;
XX DR WPI; 2000-039075/03.
XX PT Immunoglobulin-derived binding molecules that do not activate complement
XX PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
XX PT properties.
XX PS Claim 12; Fig 17; 81pp; English.
XX CC This sequence represents the mutated CH2 molecule Gidelataac, and is a
XX CC binding molecule of the invention. The recombinant binding molecule is
XX CC capable of binding a target molecule without triggering complement
XX CC dependent lysis, or the cell-mediated destruction of the target
XX CC comprises: (a) a binding domain capable of binding a target molecule; and
XX CC (b) an effector domain that is homologous to all or part of a constant
XX CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
XX CC molecule is used to bind a target molecule (especially FcgammaRIIb
XX CC causing inhibition of B cell activation, mast cell degranulation or
XX CC phagocytosis). The binding molecule can be used to prevent or inhibit the
XX CC binding of a second binding molecule, e.g. an antibody, to the target
XX CC molecule. The binding molecule is useful for the treatment of graft-vs-
XX CC host disease, organ transplant rejection, bone-marrow transplant
XX CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
XX CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
XX CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
XX CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
XX CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
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Cc coronary artery occlusion). The binding molecules do not activate
Cc complement or trigger cytotoxic activities through FcgammaR and desirable
Cc IgG properties have been retained. The polypeptides do not contain non-
Cc human amino acids, and are therefore likely to have reduced
Cc immunogenicity. Further, they still bind Protein A, which is consistent
Cc with being able to cross the human placenta through interaction with FcRn
Cc (neonatal Fc receptor)
XX SQ Sequence 110 AA;
Query Match      96.3%; Score 559.5; DB 3; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.2e-49;
Matches 108; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Db 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Qy 60 PREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 61 PREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 13
ADM33853
ID ADM33853 standard; protein; 436 AA.
XX AC ADM33853;
XX DT 03-JUN-2004 (first entry)
XX KW Human HuEPO-L-Vfcgamma2 fusion protein.
XX DE Erythropoietin; EPO; immunoglobulin; IgG;
XX KW fragment crystallisation region; FC; chronic anaemia; renal disease;
XX KW cancer chemotherapy; rheumatoid arthritis; AIDS;
XX KW myelodysplastic syndrome; (HuEPO)-L-vfcgamma2; human.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key
XX FT Location/Qualifiers
XX FT 1..27 Peptide
XX FT /note= "Signal peptide"
XX FT Protein
XX FT 28..192 /note= "EPO"
XX FT Peptide
XX FT 193..208 /note= "Linker"
XX FT Protein
XX FT 209..436 /note= "IgG2 Fc"
XX FT Misc-difference 390
XX FT /note= "Wild-type Pro substituted by Ser"
XX PN US2003082749-A1.
XX PD 01-MAY-2003.
XX PF 17-AUG-2001; 2001US-00932812.
XX PR 17-AUG-2001; 2001US-00932812.
XX PA (SUNL/) SUN L K.
XX PA (SUNB/) SUN B N C.
XX PA (SUNC/) SUN C R Y.
XX PI Sun LK, Sun BNC, Sun CRY;
XX DR WPI; 2003-616080/58.
XX PT New recombinant human erythropoietin-L-vfc fusion proteins, useful for
XX PT treating patients with chronic anemia caused by renal failure, cancer
XX PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
XX PT infection.
```



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XX      SQ      Sequence 448 AA;
Query Match          96.2%; Score 559; DB 7; Length 448;
Best Local Similarity 94.5%; Pred. No. 7.8e-49;
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0
Qy      1 APPVAGSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      233 APPVAGSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 292
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      61 REEQYNSTYRVSVSLTVLHDWLNKGKCYCKVSNKGLPSSIEKTIISRAK 109
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      293 REEQFNSTFRVSVSLTVVHDWLNKGKCYCKVSNKGLPASIEKTIISKTK 341
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: November 17, 2005, 07:04:53
Job time : 93.8333 secs

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Qy	61	REBQYNSTRVRVSVLTVLHODWLNGKEYKCKVSNKGLPSSITEKTISKAK	109
		: : : : : : : : : : : : :	
Db	281	REBQFNSTRVRVSVLTVLVHHQDWLNGKEYKCKVSNKGLPASIEKTISKTK	329
RESULT	15		
ADM33376			
ID	ADM33376	standard; protein; 448 AA.	
XX	AC	AC	
XX	ADM33376;		
DT	03-JUN-2004	(first entry)	
XX			
DE		Human GCSF-L-fragment of crystallisation gamma 2 fusion protein.	
KW		cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;	
KW		human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;	
KW		immunoglobulin G; IGG; fragment of crystallisation; immune disorder;	
KW		haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS	
KW		bone marrow transplantation; chronic neutropenia; fusion protein;	
KW		fragment of crystallisation gamma 2; FC gamma 2.	
XX			
OS	Homo sapiens.		
XX	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..30	
FT		/label= GCSF leader peptide	
FT	Protein	31..448	
FT		/note= "Mature human GCSF-L-fragment of crystallisation	
FT		gamma 2 fusion"	
FT	Misc-difference	331	
FT		/note= "Wild type Pro substituted by Ser"	
XX			
PN	US2003082679-A1.		
XX			
PD	01-MAY-2003.		
XX			
PF	01-OCT-2001; 2001US-00968362.		
XX			
PR	01-OCT-2001; 2001US-00968362.		
XX			
PA	(SUNL/) SUN L K.		
PA	(SUNB/) SUN B N C.		
PA	(SUNC/) SUN C R Y.		
PI	Sun LK, Sun BNC, Sun CRY;		
XX			
DR	WPI; 2003-595400/55.		
XX	N-PSDB; ADM33375.		
PT	New recombinant human granulocyte colony-stimulating factor (hg-CSF)-L-		
PT	vfc fusion protein for treating immune or hematopoietic system disorders		
PT	comprises hg-CSF, a flexible peptide linker, and a human immunoglobulin		
PT	FC variant.		
PS	Disclosure; Fig 2A; 15pp; English.		
XX			
CC	The invention describes a recombinant human granulocyte colony-		
CC	stimulating factor (hg-CSF)-L-vfc fusion protein comprising hg-CSF, a		
CC	peptide linker, and a human immunoglobulin G (IgG) FC variant. Also		
CC	described are: a CHO-derived cell line producing the above hg-CSF-L-vfc		
CC	fusion protein in its growth medium in excess of 10 µmrg/g per million		
CC	cells in a 24-hour period; and making the recombinant fusion protein		
CC	cited above, comprising generating a CHO-derived cell line cited above,		
CC	growing the cell line under conditions the recombinant fusion protein is		
CC	expressed in its growth medium, and purifying the expressed protein. The		
CC	recombinant fusion protein is useful in treating a variety of conditions		
CC	associated with an impaired immune or haematopoietic system, including		
CC	cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow		
CC	transplantation, and chronic neutropenias. This is the amino acid		
CC	sequence of human GCSF-L-fragment of crystallisation gamma 2 variant		
CC	fusion protein.		

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A;Contents: annotation; myeloma protein Sa, disul

R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A;Title: Structural studies of immunoglobulin G.
 A;Reference number: A93157; MUID:69064124; PMID:5782707
 A;Contents: annotation; Sa, disulfide bonds
 C;Genetics:
 A;Gene: GDB:IGHG2
 A;Cross-references: GDB:119338; OMIM:147110
 A;Map position: 14q32.33-14q32.33
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 14 hain disulfide bonds.
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;133-202/Domain: immunoglobulin homology <IM2>
 F;239-306/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (co light chain) #status experimental
 F;27-83,140-200,246-304/Disulfide bonds: #status experimental
 F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.48; Score 554; DB 1; Length 326;
 Best Local Similarity 93.6%; Pred. No. 3.2e-47;
 Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 DB 111 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170

QY 61 REQSYNSTYRVSVLTIVLHODWLNKGEYCKCKVSNKGLPSSIEKTIKAK 109
 DB 171 REQSYNSTYRVSVLTIVLHODWLNKGEYCKCKVSNKGLPAPIETISKTK 219

RESULT 2
 PT0207
 Ig gamma chain C region - chimpanzee
 C;Species: Pan troglodytes (chimpanzee)
 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 C;Accession: PT0207
 R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
 Mol. Immunol. 28, 319-322, 1991
 A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
 A;Reference number: PT0207; MUID:91287716; PMID:2062315
 A;Accession: PT0207
 A;Molecule type: mRNA
 A;Residues: 1-234 <EHR>
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;48-117/Domain: immunoglobulin homology <IMW>

Query Match 93.8%; Score 545; DB 2; Length 234;
 Best Local Similarity 91.2%; Pred. No. 1.7e-46;
 Matches 104; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55
 DB 21 PCCAPELLGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 80

QY 56 AKTKPREQVNSTYRVSVLTIVLHODWLNKGEYCKCKVSNKGLPSSIEKTIKAK 109
 DB 81 AKTKPREQVNSTYRVSVLTIVLHODWLNKGEYCKCKVSNKALPAPIETISKAK 134

RESULT 3
 S31866
 Ig gamma-1 chain C region - synthetic
 C;Species: synthetic
 A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
 C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
 C;Accession: S31866
 R;Filipula, D.
 submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene products.
 A;Reference number: S31866
 A;Accession: S31866
 A;Molecule type: mRNA
 A;Residues: 1-255 <FIL>
 A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
 C;Keywords: immunoglobulin
 F;1-22/Region: Escherichia coli outer membrane protein A precursor
 F;23-255/Region: human Ig gamma-1 chain C region

Query Match 93.5%; Score 543; DB 4; Length 255;
 Best Local Similarity 90.4%; Pred. No. 3e-46;
 Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55
 DB 35 PPCAPELLGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 94

QY 56 AKTKPREQVNSTYRVSVLTIVLHODWLNKGEYCKCKVSNKGLPSSIEKTIKAK 109
 DB 95 AKTKPREQVNSTYRVSVLTIVLHODWLNKGEYCKCKVSNKALPAPIETISKAK 148

RESULT 4
 GHU
 Ig gamma-1 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
 R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
 Nucleic Acids Res. 10, 4071-4079, 1982
 A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
 A;Reference number: A93433; MUID:82274238; PMID:6287432
 A;Accession: A93433
 A;Molecule type: DNA
 A;Residues: 1-330 <ELL>
 A;Cross-references: UNIPROT:P01857; EMBL:Z17370
 A;Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers;
 A;Note: Lys-330 is removed after translation
 R;Harris, L.J.
 submitted to the EMBL Data Library, October 1992
 A;Reference number: S33904
 A;Accession: S36861
 A;Molecule type: DNA
 A;Residues: 2-330 <HAR>
 A;Cross-references: EMBL:Z17370
 R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982
 A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A;Reference number: S33887; MUID:83001943; PMID:6811139
 A;Accession: S33887
 A;Molecule type: DNA
 A;Residues: 88-113;235-330 <TAK>
 A;Cross-references: EMBL:Z17370
 R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.
 Biochemistry 9, 3161-3170, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
 A;Reference number: A90563; MUID:71064024; PMID:5489771
 A;Contents: myeloma protein Eu
 A;Accession: B90563
 A;Molecule type: protein
 A;Residues: 1-96, 'R', 98-135 <CUN>
 A;Note: this sequence has the Gln(3) marker, 97-Arg
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
 A;Reference number: A90564; MUID:71064025; PMID:5530842
 A;Contents: Eu
 A;Accession: A90564
 A;Molecule type: protein
 A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, '
 A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
 R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A>Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), Igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: Protein

A:Residues: 1-34,'Q','K',98-115,'O','H',117-197,'D','L',199-238,'D','E',240,'L',242-268,'E',276

A>Note: This sequence has the Gln(17) and Glm(l) markers

R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A>Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI

A:Reference number: A91723; MUID:83289131; PMID:6884994

A:Contents: myeloma protein KOL; disulfide bonds

A:Accession: A91723

A:Molecule type: Protein

A:Residues: 1-96,'R','S',199-238,'E','M',242-266,'D','E',273-330 <SCH

A>Note: this sequence has the Gln(3) and Glm(non-1) markers

R:Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid

A:Reference number: A90565; MUID:71064027; PMID:4923144

A:Contents: annotation; disulfide bonds

R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A>Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobl

enbromide cleavage products, and the disulfide bridges.

A:Reference number: A91667; MUID:77070267; PMID:1002129

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IGA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:Keywords: Duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/DNA: Immunoglobulin homology <IM>

F:137-206/DNA: Immunoglobulin homology <IM>

F:243-310/DNA: Immunoglobulin homology <IM>

F:27-83,144-204,250-308/DNA: Disulfide bonds: #status experimental

F:103/disulfide bonds: interchain (to light chain) #status experimental

F:109,112/disulfide bonds: interchain (to heavy chain) #status experimental

F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 93.5%; Score 543; DB 1; Length 330;
Best Local Similarity 90.4%; Pred.No.4e-46;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 2 PP-----VAGPSVFLLPPPKPTLMISRPEVTCTVVVDVSHEDPEVKFNWYDVGVHN S5
||| : |||||
Db 110 PPCPAPELLGGSPVFLLPPPKPTLMISRPEVTCTVVVDVSHEDPEVKFNWYDVGVHN 169

Qy 56 AKTKPREEQNSTYRVSVVLTVLHQDLNCKEYKKCVSNKGLPSSIEKTISKAK 109
||||| : |||||
Db 170 AKTKPREEQNSTYRVSVVLTVLHQDLNCKEYKKCVSNKGLPAPIETISKAK 223

RESULT 5

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khmalich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995

A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

Db	175	QFNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKGLPSSIEKTSKAK	220
RESULT 7			
Ig gamma-3 chain C region (allotype G3m(b)) - human			
C/Species: Homo sapiens (man)			
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999			
C/Accession: A23511			
R/Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.			
Nucleic Acids Res. 14, 1779-1789, 1986			
A/Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cd			
A/Reference number: A23511; MUID:86148507; PMID:3081877			
A/Accession: A23511			
A/Molecule type: DNA			
A/Residues: 1-377 <HUC>			
A/Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056			
C/Genetics:			
A/Gene: GDB:IGHG3			
A/Cross-references: GDB:119339; OMIM:147120			
A/Map position: 14Q32.33-14Q32.33			
A/Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: immunoglobulin			
F;20-85/Domain: immunoglobulin homology <IMM>			
Query Match 90.2%; Score 524; DB 2; Length 377;			
Best Local Similarity 91.5%; Pred. No. 3.6e-44;			
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
QY	4	VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	63
Db	165	LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREE	224
QY	64	QYNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKGLPSSIEKTSKAK	109
Db	225	QYNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKALPAPIEKTSKTK	270
RESULT 8			
A60764			
Ig gamma-3 chain C region, form LAT - human			
C/Species: Homo sapiens (man)			
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004			
C/Accession: A60764			
R/Huck, S.; Lefranc, G.; Lefranc, M.P.			
Immunogenetics 30, 250-257, 1989			
A/Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert			
A/Reference number: A60764; MUID:90007613; PMID:2571587			
A/Accession: A60764			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-377 <HUC>			
A/Cross-references: UNIPROT:Q8N4Y9			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: immunoglobulin			
F;20-85/Domain: immunoglobulin homology <IMM>			
Query Match 90.2%; Score 524; DB 2; Length 377;			
Best Local Similarity 91.5%; Pred. No. 3.6e-44;			
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
QY	4	VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	63
Db	165	LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREE	224
QY	64	QYNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKGLPSSIEKTSKAK	109
Db	225	QYNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKALPAPIEKTSKTK	270
RESULT 9			

G3HUII			
Ig gamma-3 heavy chain disease proteins - human			
C/Species: Homo sapiens (man)			
C/Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999			
C/Accession: A90442; A92219; A90198; A93915; A02149			
R/Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.			
Biochemistry 19, 4304-4308, 1980			
A/Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-c			
A/Reference number: A90442; MUID:81021548; PMID:6774747			
A/Contents: heavy chain disease protein Wis			
A/Accession: A90442			
A/Molecule type: protein			
A/Residues: 1-289 <FRA>			
A/Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain			
A/Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 con			
A/Note: the sequence of residues 42-76 was taken from the reference that follows			
R/Michaelson, T.E.; Frangione, B.; Franklin, E.C.			
J. Biol. Chem. 252, 883-889, 1977			
A/Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication			
A/Reference number: A92219; MUID:77118561; PMID:402363			
A/Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein Wi			
A/Accession: A92219			
A/Molecule type: protein			
A/Residues: 12-97 <MIC>			
A/Note: the hinge region in gamma-3 chains is about four times as long as in other gamma			
idue segment (12-28)			
A/Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter-			
R/Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.			
Biochem. Biophys. Res. Commun. 71, 907-914, 1976			
A/Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the i			
A/Reference number: A90198; MUID:77021516; PMID:823945			
A/Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues i			
A/Accession: A90198			
A/Molecule type: protein			
A/Residues: 59-125, 'E', 128-226, 228-289 <WOL>			
A/Note: this protein lacks most of the V region, all of the CH1 region, and part of the I			
R/Alexander, A.; Steimetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;			
proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982			
A/Title: Gamma heavy chain disease in man: cDNA sequence supports partial gene deletion n			
A/Reference number: A93915; MUID:82247835; PMID:6808505			
A/Contents: heavy chain disease protein Omn			
A/Accession: A93915			
A/Molecule type: mRNA			
A/Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157,			
A/Note: a carboxyl-terminal Lys is removed posttranslationally			
A/Note: this sequence may represent an allelic form or another gamma chain subclass			
C/Comment: The heavy chain disease protein Wis is shown.			
C/Genetics:			
A/Gene: GDB:IGHG3			
A/Cross-references: GDB:119339; OMIM:147120			
A/Map position: 14Q32.33-14Q32.33			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid			
F;20-85/Domain: immunoglobulin homology <IMM>			
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental			
Query Match 86.7%; Score 504; DB 1; Length 289;			
Best Local Similarity 86.8%; Pred. No. 2.5e-42;			
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;			
QY	4	VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	63
Db	78	LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREE	137
QY	64	QYNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKGLPSSIEKTSKAK	109
Db	138	QFNSTYRVVSVLTVLHQQDMLNGKEYCKVSNKALPAPIEKTSKTK	183
RESULT 10			
147160			
Ig gamma 2b chain constant region - pig (fragment)			

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 79.8836 Seconds
(without alignments)
698.725 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVFLPPPKPDIL.....CKVSNKGLPSSIEKTIKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	554	95.4	326	1	GC2_HUMAN	P01859 homo sapien
2	554	95.4	417	2	Q6N093	Q6n093 homo sapien
3	554	95.4	465	2	Q6P6C4	Q6p6c4 homo sapien
4	551	94.8	464	2	Q6MZU6	Q6mzu6 homo sapien
5	545	93.8	493	2	Q68CN4	Q68cn4 homo sapien
6	543	93.5	330	1	GC1_HUMAN	P01857 homo sapien
7	543	93.5	348	2	Q6PTX1	Q6pyx1 homo sapien
8	543	93.5	465	2	Q6GMX6	Q6gmxx6 homo sapien
9	543	93.5	466	2	Q6IN78	Q6in78 homo sapien
10	543	93.5	469	2	Q727P5	Q7z7p5 homo sapien
11	543	93.5	470	2	Q6PJA4	Q6pja4 homo sapien
12	543	93.5	470	2	Q725W1	Q7z5w1 homo sapien
13	543	93.5	472	2	Q6N089	Q6n089 homo sapien
14	543	93.5	473	2	Q6MZV7	Q6mzv7 homo sapien
15	543	93.5	473	2	Q6P055	Q6p055 homo sapien
16	543	93.5	475	2	Q6GMW7	Q6gmw7 homo sapien
17	543	93.5	475	2	Q6MZQ6	Q6mzq6 homo sapien
18	543	93.5	475	2	Q6N095	Q6n095 homo sapien
19	543	93.5	476	2	Q6GMX1	Q6gmxx1 homo sapien
20	543	93.5	478	2	Q6P181	Q6p181 homo sapien
21	543	93.5	480	2	Q6N094	Q6n094 homo sapien
22	543	93.5	480	2	Q6PJF1	Q6pjf1 homo sapien
23	543	93.5	481	2	Q6N097	Q6n097 homo sapien
24	543	93.5	482	2	Q72351	Q7z351 homo sapien
25	543	93.5	544	2	Q6PJ95	Q6pj95 homo sapien
26	543	93.5	679	2	Q96PQ8	Q96pq8 homo sapien
27	540	92.9	327	1	GC4_HUMAN	P01861 homo sapien
28	540	92.9	466	2	Q6N096	Q6n096 homo sapien
29	540	92.9	473	2	Q8TC63	Q8tc63 homo sapien
30	538	92.6	487	2	Q652L2	Q652l2 mus sp. fv/
31	537	92.4	476	2	Q6MZX7	Q6mzx7 homo sapien

32	524	90.2	354	2	Q86TT2	Q86tt2 homo sapien
33	524	90.2	518	2	Q6N030	Q6n030 homo sapien
34	520	89.5	509	2	Q8NF17	Q8nf17 homo sapien
35	520	89.5	521	2	Q8N4Y9	Q8n4y9 homo sapien
36	504	86.7	290	1	GC3_HUMAN	P01860 homo sapien
37	443	76.2	337	2	Q95M34	Q95m34 equus caball
38	420	72.3	333	1	GC8_RAT	P20761 rattus norv
39	417	71.8	329	1	GC2_CAVPO	P01882 cavia porce
40	413	71.1	323	1	GC_RABIT	P01870 oryctolagus
41	410.5	70.7	303	2	Q6KAM2	Q6kam2 mus musculus
42	410.5	70.7	329	1	GC3_MOUSE	P22436 mus musculus
43	410.5	70.7	398	1	GC3M_MOUSE	P03987 mus musculus
44	410.5	70.7	470	2	Q7TMK1	Q7tmk1 mus musculus
45	396	68.2	324	1	GC1_MOUSE	P01868 mus musculus

ALIGNMENTS

RESULT 1

ID	GC2_HUMAN	STANDARD;	PRT;	326 AA.
AC	P01859;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	03-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ig gamma-2 chain C region.			
GN	Name=IGHG2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE OF 2-326 FROM N.A.			
RX	MEDLINE=82197621; PubMed=6804948;			
RA	Ellison J W., Hood L.E.;			
RT	"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).			
RN	[2]			
RP	SEQUENCE OF 88-115 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;			
RA	Takahashi N., Ueda S., Obata M., Nakai S., Honjo T.;			
RT	"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";			
RL	Cell 29:671-679(1982).			
RN	[3]			
RP	SEQUENCE OF 99-177 AND 310-326 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=84235992; PubMed=6329676;			
RA	Krawinkel U., Rabbitts T.H.;			
RT	"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";			
RL	EMBO J. 1:403-407(1982).			
RN	[4]			
RP	SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).			
RX	MEDLINE=81007873; PubMed=6774012;			
RA	Wang A.-C., Tung E., Fudenberg H.H.;			
RT	"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";			
RL	J. Immunol. 125:1048-1054(1980).			
RN	[5]			
RP	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).			
RX	MEDLINE=80001357; PubMed=113060;			
RA	Connell G.E., Farr D.M., Hofmann T.;			
RT	"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";			
RL	Can. J. Biochem. 57:758-767(1979).			
RN	[6]			
RP	SEQUENCE OF 238-275 (ZIE).			
RX	MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;			

RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RL immunoglobulins gamma chains";
RM Mol. Immunol. 16:923-925(1979).
RN [7].
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE) .
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8].
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RL immunoglobulins";
RM Eur. J. Biochem. 228:886-893(1995).
RN [9].
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RM Biochem. J. 121:217-225(1971).
RN [10].
RP DISULFIDE BONDS.
RX MEDLINE=69084124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RM Nature 221:145-148(1969).
RN [11].
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DR EMBL; J00230; AAB59393.1; -.
DR PIR; A93906; G2HU.
DR HSP; P01857; LOOX.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a light chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 103 103 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 140 200 Interchain (with a heavy chain).
FT DISULFID 246 304 Interchain (with a heavy chain).
FT SITE 156 156
FT VARIANT 60 60
FT At or near the complement-binding site.
FT S -> A (in myeloma proteins TIL and ZIE).
FT /FTID=VAR 003889.
FT C -> S (in Ref. 3).
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310876C6878CF9C CRC64;
Query Match 95.4%; Score 554; DB 1; Length 326;

Best Local Similarity 93.6%; Pred. No. 3.2e-46;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
DB 111 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
DB 171 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219
RESULT 2
Q6N093 PRELIMINARY; PRT; 417 AA.
AC Q6N093;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I04196 (Fragment).
GN Name=DKFZp686I04196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CAE45777.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1 1
FT SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;
Query Match 95.4%; Score 554; DB 2; Length 417;
Best Local Similarity 93.6%; Pred. No. 4.2e-46;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
DB 202 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 261
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
DB 262 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 310
RESULT 3
Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Moore T., Max S.I., Wang J., Heide F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Usdin T.B., Toshikiyuki S., Carninci P., Prange C.,
 RA Brownstein M.J., Usdin T.B., Toshikiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywanski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC062335; AA62335.1; -;
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 465 AA; 51325 MW; FDD89348AD37E6D CRC64;
 Query Match 95.4%; Score 554; DB 2; Length 465;
 Best Local Similarity 93.6%; Pred. No. 4.7e-46;
 Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 250 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 309
 Qy 61 REEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAK 109
 Db 310 REEQFNSTFRVSVLTVVHQDWLNKGYCKVSNKGLPAPIETKISTTK 358
 RESULT 4
 Q6MZU6
 ID Q6MZU6 PRELIMINARY; PRT; 464 AA.
 AC Q6MZU6
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686C15213.
 GN Name=DKFZp686C15213;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human cDNA Consortium;
 RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640874; CA845931.1; -;
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;
 Query Match 94.8%; Score 551; DB 2; Length 464;
 Best Local Similarity 92.7%; Pred. No. 9.3e-46;
 Matches 101; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 249 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 308
 Qy 61 REEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAK 109
 Db 309 REEQFNSTFRVSVLTVVHQDWLNKGYCKVSNKGLPAPIETKISTTK 357
 RESULT 5
 Q68CN4
 ID Q68CN4 PRELIMINARY; PRT; 493 AA.
 AC Q68CN4
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFZp686E3209 (Fragment).
 GN Name=DKFZp686E3209;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rectum tumor;
 RG The German cDNA Consortium;
 RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Oeanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR749861; CAH18705.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3F8AB40 CRC64;
 Query Match 93.8%; Score 545; DB 2; Length 493;

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073766; AAH73766.1; -
DR HSSP: P01861; 1ADQ.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00407; IG; 2.
DR SMART: SM00409; IG1; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 93.5%; Score 543; DB 2; Length 465;
Best Local Similarity 90.4%; Pred. No. 5.7e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDMLSRPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
|| : |||||
DB 245 PCPCAPPELLGSPSVFLFPKPKDMLSRPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 304

QY 56 AKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSSTEKTISKAK 109
|||||
DB 305 AKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSSTEKTISKAK 358

RESULT 9
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC072419; AAH72419.1; -
DR HSSP: P01861; 1ADQ.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 466 AA; 50853 MW; 53E50BCED81076E CRC64;

Query Match 93.5%; Score 543; DB 2; Length 466;
Best Local Similarity 90.4%; Pred. No. 5.7e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDMLSRPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
|| : |||||
DB 246 PCPCAPPELLGSPSVFLFPKPKDMLSRPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 305

QY 56 AKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSSTEKTISKAK 109
|||||
DB 306 AKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSSTEKTISKAK 359

RESULT 10
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.v.
Pfam; PF07654; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG.LIKE; 4.
PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 93.5%; Score 543; DB 2; Length 470;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 2 PP-----VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 55
||| : |||||
Db 249 PCPCPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 308
||| : |||||
Qy 56 AKTKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 109
||| : |||||
Db 309 AKTKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 362
||| : |||||

RESULT 11
Q6PJA4 PRELIMINARY; PRT; 470 AA.
ID Q6PJA4
AC Q6PJA4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., McKernan K.J., Farmer A.A., Rubin G.M., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR

InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.v.
Pfam; PF07654; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG.LIKE; 4.
PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 93.5%; Score 543; DB 2; Length 469;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 2 PP-----VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 55
||| : |||||
Db 249 PCPCPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 308
||| : |||||
Qy 56 AKTKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 109
||| : |||||
Db 309 AKTKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 362
||| : |||||

RESULT 11
Q6PJA4 PRELIMINARY; PRT; 470 AA.
ID Q6PJA4
AC Q6PJA4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., McKernan K.J., Farmer A.A., Rubin G.M., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR

InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR Strausberg R.;
DR EMBL; BC051328; AAH51328.1; --
DR Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 93.5%; Score 543; DB 2; Length 469;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
Qy 2 PP-----VAGPSVFPPPKKDTLMISRTPEVTCCVVVDVSHEDDEVKFNWYVDGVEVHN 55
Db 249 PCPCPELLGGSPVFLFPFKPKDTLMISRTPEVTCCVVVDVSHEDDEVKFNWYVDGVEVHN 308

Qy 56 AKTKPREEQNSTYRVSVSLTVLHQDLNGKEYCKVSKNGLPSSIETISKAK 109
Db 309 AKTKPREEQNSTYRVSVSLTVLHQDLNGKEYCKVSKNGLPSSIETISKAK 362

RESULT 11
Q6PJAA PRELIMINARY; PRT; 470 AA.

ID Q6PJAA AC Q6PJAA DT 05-JUL-2004 (TrEMBLrel. 27, Created)
AC Q6PJAA DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Soares M.B., Donald M.P., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; --
RL HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.V.

InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR Strausberg R.;
DR EMBL; BC051328; AAH51328.1; --
DR Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 469 AA; 51395 MW; CB05BE12BAAF795C CRC64;

Query Match 93.5%; Score 543; DB 2; Length 469;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
Qy 2 PP-----VAGPSVFPPPKKDTLMISRTPEVTCCVVVDVSHEDDEVKFNWYVDGVEVHN 55
Db 249 PCPCPELLGGSPVFLFPFKPKDTLMISRTPEVTCCVVVDVSHEDDEVKFNWYVDGVEVHN 308

Qy 56 AKTKPREEQNSTYRVSVSLTVLHQDLNGKEYCKVSKNGLPSSIETISKAK 109
Db 309 AKTKPREEQNSTYRVSVSLTVLHQDLNGKEYCKVSKNGLPSSIETISKAK 362

RESULT 11
Q6PJAA PRELIMINARY; PRT; 470 AA.

ID Q6PJAA AC Q6PJAA DT 05-JUL-2004 (TrEMBLrel. 27, Created)
AC Q6PJAA DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Soares M.B., Donald M.P., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; --
RL HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.V.

```

DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match          93.5%; Score 543; DB 2; Length 470;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
   ||| : |||||
DB 250 PCPAPPELLGGPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 309
   ||| : |||||

QY 56 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
   ||||| : |||||
DB 310 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 363
   ||||| : |||||

RESULT 13
Q6N089
ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFp686P15220.
GN Name=DKFp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB34D0D046D279 CRC64;

Query Match          93.5%; Score 543; DB 2; Length 472;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
   ||| : |||||
DB 252 PCPAPPELLGGPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 311
   ||| : |||||

QY 56 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
   ||||| : |||||
DB 312 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365
   ||||| : |||||

RESULT 14
Q6MZV7
ID Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFp686C11235.
GN Name=DKFp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4C0BFC447 CRC64;

Query Match          93.5%; Score 543; DB 2; Length 473;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
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DB 253 PCPAPPELLGGPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 312
   ||| : |||||

QY 56 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
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DB 313 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 366
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RESULT 15
Q6P055
ID Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -;
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig Cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-Bet; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 93.5%; Score 543; DB 2; Length 473;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy	2	PP-----VAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
Db	253	PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 312
Qy	56	AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db	313	AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 366

Search-completed: November 17, 2005, 07:10:19
Job time : 81.8836 secs

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, STATE: MA
, COUNTRY: USA
, ZIP: 02173
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, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/444,644
, FILING DATE:
, CLASSIFICATION: 424
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/232,246
, FILING DATE: 07-JUL-1994
, PRIOR APPLICATION NUMBER:
, APPLICATION NUMBER: US 07/800,458
, FILING DATE: 26-NOV-1991
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: PCT/US90/05077
, FILING DATE: 07-SEP-1989
, ATTORNEY/AGENT INFORMATION:
, NAME: Wagner, Richard W.
, REGISTRATION NUMBER: 34,480
, REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (617) 861-6240
, TELEFAX: (617) 861-9540
, INFORMATION FOR SEQ ID NO: 30:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 109 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, FRAGMENT TYPE: internal
, US-08-444-644-30

Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKTK 109

RESULT 3
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6323508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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, CITY: Lexington
, STATE: MA
, COUNTRY: USA
, ZIP: 02173
, COMPUTER READABLE FORM:
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, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
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, FILING DATE:
, CLASSIFICATION: 424
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/232,246
, FILING DATE: 07-JUL-1994
, PRIOR APPLICATION NUMBER:
, APPLICATION NUMBER: US 07/800,458
, FILING DATE: 26-NOV-1991
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: PCT/US90/05077
, FILING DATE: 07-SEP-1989
, ATTORNEY/AGENT INFORMATION:
, NAME: Wagner, Richard W.
, REGISTRATION NUMBER: 34,480
, REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (617) 861-6240
, TELEFAX: (617) 861-9540
, INFORMATION FOR SEQ ID NO: 30:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 109 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, FRAGMENT TYPE: internal
, US-08-444-644-30

Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKTK 109

RESULT 4
US-09-483-588-5
; Sequence 5, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/09/483,588
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: US 60/116,023
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-483-588-5

Query Match 95.4%; Score 554; DB 4; Length 217;
Best Local Similarity 93.6%; Pred. No. 5.9e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
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/ ADDRESSEE: Cooper & Dunham
/ STREET: 30 Rockefeller Plaza
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10112
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.24
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/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/477,450
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: US 07/927,931
/ FILING DATE: 07-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
/ TELEPHONE: (212) 977-9550
/ TELEFAX: (212) 977-9809
/ TELEX: 422523 COOP UI
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 432 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: homo sapien
/ CELL TYPE: lymphocyte
/ US-09-329-916-2

Query Match 95.4%; Score 554; DB 3; Length 432;
Best Local Similarity 93.8%; Pred. No. 1.4e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLFPKPKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPKPKDTLMISRPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
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Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 9
US-08-485-372A-2
; Sequence 2, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.24
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/ APPLICATION NUMBER: US/08/485,372A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/476,227
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 37690-II-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 432 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: homo sapien
/ CELL TYPE: lymphocyte
/ US-08-485-372A-2

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Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 10
US-09-409-006A-2
; Sequence 2, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/409,006A
/ FILING DATE: 29-SEP-1999
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/927,931
/ FILING DATE: 07-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-409-006A-2

Query Match 95.4%; Score 554; DB 3; Length 432;
Best Local Similarity 93.6%; Pred. No. 1.4e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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Db 277 REEQFNSTFRVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 11

US-08-484-681-2
Sequence 2, Application US/08484681
Patent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-484-681-2

Query Match 95.4%; Score 554; DB 4; Length 432;
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Db 277 REEQFNSTFRVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 12

US-09-766-995-2
Sequence 2, Application US/09766995
Patent No. 6737267
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: homo sapians
US-09-766-995-2

Query Match 95.4%; Score 554; DB 4; Length 432;
Best Local Similarity 93.6%; Pred. No. 1.4e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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Qy 61 REEQYNSTYRVSVLTVLVHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
Db 277 REEQFNSTFRVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 13

PCT-US93-07422-2
Sequence 2, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA: US 07/927,931
FILING DATE: 07-AUG-1992

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 977-9550
/ TELEFAX: (212) 977-9809
/ TELEX: 422523 COOP UI
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 432 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: homo sapien
/ CELL TYPE: lymphocyte
PCT-US93-07422-2

Query Match 95.4%; Score 554; DB 5; Length 432;
Best Local Similarity 93.6%; Pred. No. 1.4e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Db 217 APPVAGPSVFLPPPKPDTLMISRTPETVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276

QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
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RESULT 14

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/ Sequence 70, Application US/09472087
/ Patent No. 6682736
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, ELLEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1
/ CURRENT APPLICATION NUMBER: US/09/472,087
/ CURRENT FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 60/113,647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 70
/ LENGTH: 451
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-472-087-70

Query Match 95.4%; Score 554; DB 4; Length 451;
Best Local Similarity 93.6%; Pred. No. 1.5e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 236 APPVAGPSVFLPPPKPDTLMISRTPETVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 295

QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 296 REEQFNSTFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 344
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RESULT 15

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US-09-472-087-1
/ Sequence 1, Application US/09472087
/ Patent No. 6682736
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, ELLEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1
/ CURRENT APPLICATION NUMBER: US/09/472,087
/ CURRENT FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 60/113,647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-472-087-1

Query Match 95.4%; Score 554; DB 4; Length 463;
Best Local Similarity 93.6%; Pred. No. 1.6e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 248 APPVAGPSVFLPPPKPDTLMISRTPETVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 307

QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 308 REEQFNSTFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 356

Search completed: November 17, 2005, 07:13:20
Job time : 25.3881 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 83.6164 Seconds
(without alignments)
545.427 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTIKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	581	100.0	329	20	US-11-102-403-25
2	573	98.6	109	18	US-10-959-318-11
3	573	98.6	109	18	US-10-959-318-12
4	567	97.5	449	16	US-10-493-676-11
5	565	97.2	472	14	US-10-006-593-67
6	565	97.2	472	15	US-10-307-724-67
7	565	97.2	472	12	US-10-737-290-67
8	562.5	96.8	110	18	US-10-959-318-9
9	562.5	96.8	110	18	US-10-959-318-10
10	562	96.7	447	16	US-10-745-775-16
11	559	96.2	109	18	US-10-959-318-15
12	559	96.2	109	18	US-10-959-318-16
13	559	96.2	109	18	US-10-959-318-17
14	559	96.2	109	18	US-10-959-318-18
15	559	96.2	109	18	US-10-959-318-19
16	559	96.2	109	18	US-10-959-318-20
17	559	96.2	109	18	US-10-959-318-21
18	559	96.2	109	18	US-10-959-318-22
19	559	96.2	109	18	US-10-959-318-23
20	559	96.2	109	18	US-10-959-318-24
21	559	96.2	109	18	US-10-959-318-25
22	559	96.2	109	18	US-10-959-318-26
23	559	96.2	109	18	US-10-959-318-27
24	559	96.2	109	18	US-10-959-318-28
25	559	96.2	109	18	US-10-959-318-29
26	559	96.2	109	18	US-10-959-318-30
27	559	96.2	109	18	US-10-959-318-31
28	559	96.2	109	18	US-10-959-318-32
29	559	96.2	109	18	US-10-959-318-33
30	559	96.2	109	18	US-10-959-318-34
31	559	96.2	109	18	US-10-959-318-35
32	559	96.2	109	18	US-10-959-318-36
33	559	96.2	109	18	US-10-959-318-37
34	559	96.2	109	18	US-10-959-318-38
35	559	96.2	109	18	US-10-959-318-39
36	559	96.2	109	18	US-10-959-318-40
37	559	96.2	109	18	US-10-959-318-41
38	559	96.2	109	18	US-10-959-318-42
39	559	96.2	109	18	US-10-959-318-43
40	559	96.2	109	18	US-10-959-318-44
41	559	96.2	109	18	US-10-959-318-45
42	559	96.2	109	18	US-10-959-318-46
43	559	96.2	109	18	US-10-959-318-47
44	559	96.2	109	18	US-10-959-318-48
45	559	96.2	109	18	US-10-959-318-49

Query Match 100.0%; Score 581; DB 20; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;

ALIGNMENTS

RESULT 1

US-11-102-403-25
; Sequence 25, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PARRIN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STREIN, PAMELA
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-25


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; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67

Query Match          97.2%; Score 565; DB 14; Length 472;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 257 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316
QY 61 REEQNSTYRVSVSLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 109
Db 317 REEQNSTYRVSVSLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 365

RESULT 6
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

Query Match          97.2%; Score 565; DB 15; Length 472;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 257 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316
QY 61 REEQNSTYRVSVSLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 109
Db 317 REEQNSTYRVSVSLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 365

RESULT 7
US-10-307-7290-67
; Sequence 67, Application US/10737290

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; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orecchia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-737-290-67

Query Match          97.2%; Score 565; DB 16; Length 472;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 257 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316
QY 61 REEQNSTYRVSVSLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 109
Db 317 REEQNSTYRVSVSLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 365

RESULT 8
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-9

Query Match          96.8%; Score 562.5; DB 18; Length 110;
Best Local Similarity 98.2%; Pred. No. 2e-47;

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-16

Query Match 96.2%; Score 559; DB 18; Length 109;
Best Local Similarity 96.3%; Pred. No. 4.4e-47;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 109

RESULT 13
US-09-932-812-18
; Sequence 18, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932.812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: A)
US-09-932-812-18

Query Match 96.2%; Score 559; DB 10; Length 436;
Best Local Similarity 94.5%; Pred. No. 2.1e-46;
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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Db 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 280
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 281 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTIISKTK 329

RESULT 14
US-10-761-593A-18
; Sequence 18, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological activity
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812

; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: 2A)
US-10-761-593A-18

Query Match 96.2%; Score 559; DB 16; Length 436;
Best Local Similarity 94.5%; Pred. No. 2.1e-46;
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 280
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 281 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTIISKTK 329

RESULT 15
US-11-016-518A-18
; Sequence 18, Application US/11016518A
; Publication No. US20050124045A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity
; FILE REFERENCE: 02SUN2004D1
; CURRENT APPLICATION NUMBER: US/11/016,518A
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US 09/932,812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: 2A)
US-11-016-518A-18

Query Match 96.2%; Score 559; DB 20; Length 436;
Best Local Similarity 94.5%; Pred. No. 2.1e-46;
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 280
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 281 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTIISKTK 329

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Job time : 84.6164 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.0913 Seconds
(without alignments)
473.187 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVLFPPPKPQDTL.....CKVSNKGLPSSIKTISKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: Geneseqp1980s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	554	95.4	109	3	AAY54997 Mutated C
5	542	93.3	109	7	Add25659 Binding d
6	542	93.3	110	2	AAR27680 Human imm
7	542	93.3	110	2	AAR41684 Undefined
8	542	93.3	110	8	ADH75385 Human IGG
9	541	93.1	105	2	AAY42626 Human IGG
10	540	92.9	109	2	AAR67438 OXK3 mono
11	540	92.9	110	2	AAR41717 Undefined
12	537	92.4	109	5	AAE28089 Human imm
13	537	92.4	110	8	ADH75415 CH2 regio
14	536	92.3	110	8	ADL90103 Human imm
15	535	92.1	110	8	ADH75413 CH2 regio
16	534	91.9	109	7	Add25761 Binding d
17	528	90.9	102	8	ADJ52129 CH1 delet
18	526	90.5	102	8	ADJ52132 CH1 delet
19	518	89.2	110	2	AAR41713 Undefined
20	408	70.2	110	2	AAW71023 Mus muscu
21	382	65.7	110	1	AAP83207 Sequence
22	344	59.2	72	8	ADL15711 Human imm
23	329	56.6	66	2	AAR75349 C-gamma-1
24	329	56.6	66	2	AAR75351 C-gamma-1
25	305	52.5	76	8	ADL15713 Human imm

26	270	46.5	56	1	AAP83205 Sequence
27	269.5	46.4	56	1	AAP83204 Sequence
28	266	45.8	56	1	AAP83201 Sequence
29	266	45.8	56	1	AAP83202 Sequence
30	265.5	45.7	56	1	AAP83203 Sequence
31	264.5	45.5	56	1	AAP83206 Sequence
32	249	42.9	46	8	ADR59138 Human IGG
33	234	40.3	46	8	ADR59139 Human IGG
34	232.5	40.0	110	2	AAR33315 Variant I
35	221	38.0	46	8	ADR59142 Rhesus mo
36	215	37.0	46	8	ADR59143 Rhesus mo
37	209	36.0	46	8	ADR59140 Rhesus mo
38	209	36.0	46	8	ADR59141 Crab-eati
39	203.5	35.0	110	2	AAR33314 Variant I
40	201.5	34.7	110	2	AAR33316 Variant I
41	199	34.3	96	3	AAB53640 Human col
42	198	34.1	46	8	ADR59148 Camel IGG
43	194	33.4	46	8	ADR59145 Pig IGG2a
44	193.5	33.3	110	2	AAR33693 Variant I
45	192	33.0	46	8	ADR59147 Llama IGG

ALIGNMENTS

RESULT 1

AAV54996

ID AAY54996 standard; protein; 109 AA.

AC AAY54996;

XX

DT 17-FEB-2000 (first entry)

XX

DE Mutated CH2 sequence G1deltaaab.

XX

XX

KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;

KW cell-mediated destruction; human; immunoglobulin G; IGG heavy chain;

KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;

KW Crohn's disease; graft-vs-host disease; organ transplant rejection;

KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;

KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;

KW neonatal alloimmune thrombocytopenia; arthritis; erythroblastosis foetalis;

KW sickle cell anaemia; coronary artery occlusion.

XX

OS Synthetic.

XX

PN WO958572-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001441.

XX

PR 08-MAY-1998; 98GB-00009951.

XX

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX

PI Armour KL, Clark MR, Williamson LM;

XX

DR WPI; 2000-039075/03.

XX

PT Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

PT

XX Claim 12; Fig 17; 81pp; English.

PS

CC This sequence represents the mutated CH2 molecule G1deltaaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target

CC comprises: (a) a binding domain capable of binding a target molecule; and

CC (b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcgammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of graft-vs-
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain non-
 CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)
 XX
 SQ Sequence 109 AA;
 Query Match 100.0%; Score 581; DB 3; Length 109;
 Best Local Similarity 100.0%; Pred. No. 7.5e-52;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 60
 DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 60
 QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
 DB 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
 RESULT 2
 AAY54998
 ID AAY54998 standard; protein; 110 AA.
 XX
 AC AAY54998;
 XX
 DT 17-FEB-2000 (first entry)
 DE Mutated CH2 sequence G1deltaaac.
 XX
 KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmunity; asthma; allergy;
 KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.
 XX
 OS Synthetic.
 XX
 PN WO9958572-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-GB001441.
 PR 08-MAY-1998; 98GB-00009951.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Armour KL, Clark MR, Williamson LM;
 DR WPI; 2000-039075/03.
 XX
 PT Immunoglobulin-derived binding molecules that do not activate complement
 or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.
 XX Claim 12; Fig 17; 81pp; English.
 PS
 CC This sequence represents the mutated CH2 molecule G1deltaaac, and is a
 CC binding molecule of the invention. The recombinant binding molecule is
 CC capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain non-
 CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)
 XX
 SQ Sequence 110 AA;
 Query Match 96.3%; Score 559.5; DB 3; Length 110;
 Best Local Similarity 98.2%; Pred. No. 1.2e-49;
 Matches 108; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
 DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 QY 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
 DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 RESULT 3
 AAR41709
 ID AAR41709 standard; protein; 109 AA.
 XX
 AC AAR41709;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-OCT-1993 (first entry)
 XX
 DE Undefined ORF2 encoded by plasmid pAH4625.
 XX
 KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
 KW light; chain; variable; constant; region; anti-human; pAH4807;
 KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
 KW endothelial cell; conjugate; neuropharmacological; gamma-3; gamma-4;
 KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
 KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
 XX
 OS Synthetic.
 XX
 PN WO9310819-A1.
 XX
 PD 10-JUN-1993.
 XX
 PF 24-NOV-1992; 92WO-US010206.
 XX
 PR 26-NOV-1991; 91US-00800458.
 XX

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PA (ALKE-) ALKERMES INC.
XX
XX Friden PM;
XX
XX WPI: 1993-196742/24.
XX N-PSDB; AAQ43846.
XX
XX Antibody conjugates specific for transferrin receptor - used for
XX diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
XX Disclosure; Fig 17J; 151pp; English.
XX
XX The sequences given in AA411707-09 are encoded by the expression vector
XX pAH4625. This vector represents the cloning of the human gamma isotype,
XX gamma-2, with the variable region of the murine monoclonal antibody
XX 128.1. This plasmid encodes a chimeric monoclonal antibody in which the
XX heavy chain (VH) is derived from a murine source and the sequences
XX encoding CH1, CH2 and CH3 are derived from a human source. This vector,
XX in combination with the chimeric light chain vector, pA4611 (see also
XX AAQ43845), was transfected into SP2/0 cells and clones were isolated.
XX 128.1 is an anti-human transferrin receptor antibody which binds to the
XX transferrin receptor on brain capillary endothelial cells. This antibody
XX may be used in a conjugate in which it is linked to a neuropharmaceutical
XX or diagnostic agent. The conjugate may be used to treat or prevent
XX neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
XX Parkinsons and Alzheimers disease. It may also be used for diagnostic
XX methods. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 109 AA;
XX
XX Query Match 95.4%; Score 554; DB 2; Length 109;
XX Best Local Similarity 93.6%; Pred. No. 4.5e-49;
XX Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 APPVAGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 APPVAGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
XX
XX Qy 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 REQQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIKTK 109
XX
XX RESULT 4
XX ID AA54997
XX AC AA54997
XX
XX DT 17-FEB-2000 (first entry)
XX
XX DE Mutated CH2 sequence G2deltaa.
XX
XX KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
XX cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
XX B cell activation; mast cell degranulation; phagocytosis; vasculitis;
XX Crohn's disease; graft-vs-host disease; organ transplant rejection;
XX bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
XX autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
XX autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis;
XX neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy;
XX sickle cell anaemia; coronary artery occlusion.
XX
XX OS Synthetic.
XX
XX PN W09958572-A1.
XX
XX PD 18-NOV-1999.
XX
XX PF 07-MAY-1999; 99WO-GB001441.
XX
XX PR 08-MAY-1998; 98GB-00009951.
XX
XX

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PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Armour KL, Clark MR, Williamson LM;
XX
XX WPI: 2000-039075/03.
XX
XX Immunoglobulin-derived binding molecules that do not activate complement
XX or trigger cytotoxic activities and maintaining desirable immunoglobulin
XX properties.
XX
XX Claim 12; Fig 17; 81pp; English.
XX
XX This sequence represents the mutated CH2 molecule G2deltaa, and is a
XX binding molecule of the invention. The recombinant binding molecule is
XX capable of binding a target molecule without triggering complement
XX dependent lysis, or the cell-mediated destruction of the target
XX comprises: (a) a binding domain capable of binding a target molecule; and
XX (b) an effector domain that is homologous to all or part of a constant
XX domain of a human immunoglobulin G (IgG) heavy chain. The binding
XX molecule is used to bind a target molecule (especially FcgammaRIIb
XX causing inhibition of B cell activation, mast cell degranulation or
XX phagocytosis). The binding molecule can be used to prevent or inhibit the
XX binding of a second binding molecule, e.g. an antibody, to the target
XX molecule. The binding molecule is useful for the treatment of graft-vs-
XX host disease, organ transplant rejection, bone-marrow transplant
XX rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
XX autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g.
XX foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy),
XX chronic or acute inflammatory diseases (e.g. Crohn's, HDN
XX (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
XX coronary artery occlusion). The binding molecules do not activate
XX complement or trigger cytotoxic activities through FcgammaRIIb and desirable
XX IgG properties have been retained. The polypeptides do not contain non-
XX human amino acids, and are therefore likely to have reduced
XX immunogenicity. Further, they still bind Protein A, which is consistent
XX with being able to cross the human placenta through interaction with FcRn
XX (neonatal Fc receptor)
XX
XX Sequence 109 AA;
XX
XX Query Match 95.4%; Score 554; DB 3; Length 109;
XX Best Local Similarity 94.5%; Pred. No. 4.5e-49;
XX Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 APPVAGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 APPVAGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
XX
XX Qy 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 REQQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
XX
XX RESULT 5
XX ID ADD25659
XX AC ADD25659
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Binding domain-immunoglobulin fusion protein-associated protein #107.
XX
XX KW Binding domain; immunoglobulin; fusion protein; cytostatic;
XX antiarthritis; immunosuppressive; antidiabetic; antithyroid;
XX neuroprotective; hinge region; immunoglobulin heavy chain;
XX CH2 constant region; CH3 constant region; IgG1;
XX antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
XX rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
XX OS Unidentified.

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XX US2003118592-A1.
XX 26-JUN-2003.
XX 25-JUL-2002; 2002US-00207655.
XX 17-JAN-2001; 2001US-0367358P.
XX 17-JAN-2002; 2002US-00053530.
XX 03-JUN-2002; 2002US-0385691P.
XX (GENE-) GENE-CRAFT INC.
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WPI; 2003-801317/75.
XX New binding domain-immunoglobulin fusion protein, useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX Disclosure; SEQ ID NO 220; 157pp; English.
XX The invention relates to a binding domain-immunoglobulin fusion protein
XX comprising a binding domain polypeptide that is fused to an
XX immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CH2 constant region polypeptide that is fused to the hinge region
XX polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX polypeptide that is fused to the CH2 constant region polypeptide. The
XX hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
XX hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
XX region polypeptide, derived from (a) having 3 or more cysteine residues;
XX where the mutated human IgG1 immunoglobulin hinge region polypeptide
XX contains 2 cysteine residues, where the first cysteine is not mutated; a
XX mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
XX (a) having 3 or more cysteine residues, where the mutated human IgG1
XX immunoglobulin hinge region polypeptide contains no more than one
XX cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
XX polypeptide, derived from (a) having 3 or more cysteine residues; where
XX the mutated human IgG1 immunoglobulin hinge region polypeptide contains
XX no cysteine residues. The binding domain-immunoglobulin fusion protein is
XX capable of at least one immunological activity comprising antibody
XX dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
XX binding domain polypeptide is capable of specifically binding to an
XX antigen. Also included are an isolated polynucleotide encoding the
XX binding domain-immunoglobulin fusion protein, a recombinant expression
XX construct comprising the polynucleotide (operably linked to a promoter),
XX a host cell transformed or transfected with a recombinant expression
XX construct, producing the binding domain-immunoglobulin fusion protein, a
XX pharmaceutical composition comprising the binding domain-immunoglobulin
XX fusion protein or polynucleotide and a carrier, and treating a subject
XX having or suspected of having a malignant condition or a B-cell disorder.
XX The binding domain-immunoglobulin fusion protein is useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
XX myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
XX sclerosis or autoimmune disease. The present sequence is a binding domain
XX -immunoglobulin fusion protein-associated protein sequence. Note: The
XX sequence data for this patent formed part of the printed specification
XX and is also available in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docid=20030118592. The authors have not
XX identified the sequences in the printed specification by their SEQ ID
XX number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 109 AA;
Query Match 93.3%; Score 542; DB 7; Length 109;
Best Local Similarity 95.3%; Pred. No. 7.8e-48;
Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 63
Db 4 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 63

QY 64 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 64 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 6
AAR27680
ID AAR27680 standard; protein; 110 AA.
XX AAR27680;
AC AAR27680;
XX 25-MAR-2003 (revised)
DT 10-MAR-1993 (first entry)
XX Human immunoglobulin IgG1 CH2 region.
XX Isoallotype; IgG1 G1m(1,2,17); anti-allotype response; humanised Ab.
XX Homo sapiens.
XX WO9216562-A1.
XX 01-OCT-1992.
XX 12-MAR-1992; 92WO-GB000445.
XX 12-MAR-1991; 91GB-00005245.
XX (LYNX-) LYNXVALE LTD.
XX Clark MR;
XX WPI; 1992-349162/42.
XX Humanised antibodies having modified allotypic determinant - useful for
XX matching allotypes in therapy with decreased likelihood of causing
XX undesirable immune responses.
XX Disclosure; Fig 4c; 57pp; English.
XX In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.
XX The inventor's propose eliminating these allotypes by amino acid changes
XX to agree with the sequences of IG32, IG3 and IG4. None of the allotype
XX sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes"
XX should be suitable for therapeutic use in all patients. See AAR27678-
XX R27681. (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 110 AA;
Query Match 93.3%; Score 542; DB 2; Length 110;
Best Local Similarity 95.3%; Pred. No. 7.9e-48;
Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 63
Db 5 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 64

QY 64 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 65 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 7
AAR41684
ID AAR41684 standard; protein; 110 AA.
XX AAR41684;
XX 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX Undefined ORF2 encoded by pAH4602.

XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;
 KW chain; variable; constant; region; anti-human; transferrin; receptor;
 KW antibody; brain; capillary; endothelial cell; conjugate;
 KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke; epilepsy;
 KW Parkinsons disease; Alzheimers disease.
 XX Synthetic.
 XX WO9310819-A1.
 XX 10-JUN-1993.
 XX 24-NOV-1992; 92WO-US010206.
 XX 26-NOV-1991; 91US-00800458.
 XX (ALKE-) ALKERMES INC.
 XX Friden PM;
 XX WPI; 1993-196742/24.
 XX N-PSDB; AAQ43844.
 XX Antibody conjugates specific for transferrin receptor - used for
 PT diagnosis and treatment of cancer, AIDS and neurological disorders.
 XX Disclosure; Fig 11K; 151pp; English.
 CC The sequences given in AAR41682-85 are encoded by the expression vector,
 CC pAH4602. This vector contains open reading frames encoding the heavy
 CC chain variable region (VH) of the antibody 128.1, an ampicillin
 CC resistance gene and a histidine (histidinol) selection marker.
 CC Transcription of the VH gene is from the VH promoter of the murine 27.44
 CC gene. The vector also includes a heavy chain immunoglobulin enhancer and
 CC the human gammal constant region (CH). The VH region of 128.1 was
 CC isolated by polymerase chain reaction and cloned into plasmid pAH4274.
 CC This was achieved by digesting the plasmid and the product with EcoRV and
 CC NheI. The VH gene was inserted in-frame with the human gammal CH region
 CC CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an
 CC anti-human transferrin receptor antibody which binds to the transferrin
 CC receptor on brain capillary endothelial cells. This antibody may be used
 CC in a conjugate in which it is linked to a neuro- pharmaceutical or
 CC diagnostic agent. The conjugate may be used to treat or prevent
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 110 AA;
 SQ Query Match 93.3%; Score 542; DB 2; Length 110;
 Best Local Similarity 95.3%; Pred. No. 7.9e-48;
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 VAGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 63
 Db : |||||
 5 LGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 64
 QY 64 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 Db : |||||
 65 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110
 RESULT 8
 ADH75385
 ID ADH75385 standard; protein; 110 AA.
 XX AC ADH75385;
 XX 22-APR-2004 (first entry)
 XX Human IgG1 CH2 region.
 DE

KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
 KW autoimmune disease; human; IgG; immunoglobulin.
 XX Homo sapiens.
 OS US2004002587-A1.
 PN 01-JAN-2004.
 PD 20-FEB-2003; 2003US-00370749.
 XX 20-FEB-2002; 2002US-0358161P.
 XX (WATK/) WATKINS J D.
 PA (ALLA/) ALLAN B.
 XX Watkins JD, Allan B;
 PI WPI; 2004-070755/07.
 DR New composition comprising a variant of a parent polypeptide having at
 XX least a portion of a Fe region, useful in treating e.g., autoimmune
 PT diseases.
 PS Claim 20; SEQ ID NO 23; 62pp; English.
 XX The invention relates to a new composition comprises a variant of a
 CC parent polypeptide having at least a portion of a Fc region. The variant
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
 CC presence of effector cells more effectively than the parent polypeptide
 CC and comprises at least one amino acid modification at position 280 in the
 CC Fc region. The composition is useful in treating diseases e.g.,
 CC autoimmune diseases. The present sequence represents the amino acid
 CC sequence of a human immunoglobulin G, IgG, CH region.
 XX Sequence 110 AA;
 SQ Query Match 93.3%; Score 542; DB 8; Length 110;
 Best Local Similarity 95.3%; Pred. No. 7.9e-48;
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 VAGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 63
 Db : |||||
 5 LGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 64
 QY 64 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 Db : |||||
 65 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110
 RESULT 9
 AAY42626
 ID AAY42626 standard; protein; 105 AA.
 XX AC AAY42626;
 XX 10-JAN-2000 (first entry)
 XX Human IgG1 Fc gamma1-Fc gamma2 residues.
 XX Immunoglobulin E; IgE; antagonist; Fc epsilon RI receptor; human; bds;
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;
 KW allergic disease.
 XX Homo sapiens.
 OS US5965709-A.
 PN 12-OCT-1999.
 PD 21-APR-1994; 94US-00232539.
 XX 14-AUG-1991; 91US-00744768.
 PR

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:37:49 ; Search time 16.4247 Seconds
(without alignments)
638.529 Million cell updates/sec

Title: US-09-674-857-1
Perfect score: 581
Sequence: 1 APPVAGSFLFPKPKDTL.....CKVSNKGLPSSIEKTISKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 44790

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276	47.5	88	2 A30503	Ig gamma-2b chain
2	141	24.3	107	2 I68726	IgE chain C3 regio
3	139	23.9	106	1 K3HU	Ig kappa chain C r
4	138	23.8	107	2 I68730	IgE chain C3 regio
5	134	23.1	99	2 S26553	Ig kappa chain C r
6	133.5	23.0	105	2 B30554	Ig lambda chain C
7	132	22.7	103	2 B26167	Ig lambda chain C
8	131.5	22.6	105	2 B26434	Ig lambda-5 chain
9	130	22.4	110	2 S43147	Ig epsilon chain -
10	127.5	21.9	105	1 L1MS	Ig lambda-1 chain
11	127.5	21.9	106	2 S22760	Ig lambda-2 chain
12	126.5	21.8	106	2 S00259	Ig lambda-5 chain
13	118.5	20.4	105	1 L2HU	Ig lambda chain C
14	118.5	20.4	105	2 H32529	Ig lambda chain C
15	117.5	20.2	98	2 S26654	Ig lambda chain C
16	116.5	20.1	104	2 P53275	Ig kappa-1 chain C
17	115	19.8	99	2 A37927	Ig kappa chain C r
18	114	19.6	102	2 B34509	Ig kappa chain C r
19	113.5	19.5	109	1 L7RB	Ig lambda chain C
20	112.5	19.4	103	1 K4RB	Ig kappa-B4 chain
21	110	18.9	106	2 I50741	Ig lambda chain -
22	110	18.9	106	2 I50740	Ig lambda chain C
23	108.5	18.7	105	1 L1PG	Ig lambda chain C
24	108	18.6	105	2 A27390	Ig lambda-1 chain
25	107	18.4	106	1 K1MS	Ig kappa chain C r
26	104	17.9	104	1 K5RBV	Ig kappa chain C r
27	102.5	17.6	102	2 I46731	lambda-chain C-reg
28	99	17.0	105	2 B27390	Ig lambda-2 chain
29	99	17.0	106	1 K1RTB	Ig kappa chain C r

30 99 17.0 106 1 K4RBBS
31 99 17.0 106 2 G20907
32 94 16.2 104 1 L3MS
33 94 16.2 105 2 S22762
34 94 16.2 106 1 K1RTA
35 93 16.0 104 1 K9RB
36 92 15.8 103 1 K5RB
37 85 14.6 97 2 S26652
38 83.5 14.4 78 2 C34509
39 80 13.8 82 2 I57802
40 80 13.8 104 1 L2MS
41 80 13.8 105 2 S22759
42 79.5 13.7 78 2 D34509
43 76.5 13.2 67 2 PLO186
44 64.5 11.1 107 2 I68725
45 64 11.0 90 2 A24629

ALIGNMENTS

RESULT 1

A30503 Ig gamma-2b chain C region (B5.7A12) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C;Accession: A30503

R;Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.

J. Immunol. 141, 1754-1761, 1988

A;Title: DNA rearrangements affecting both variable and constant regions of Ig H chain g

A;Reference number: A30503; MUID:88315788; PMID:2842402

A;Accession: A30503

A;Molecule type: mRNA

A;Residues: 1-88 <GIL>

A;Cross-references: GB:M21925

A;Experimental source: myeloma cell line MPC11

A;Note: the authors translated the codon GAG for residue 41 as Ser

C;Genetics:

A;Introns: 46/3

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;1-70/Domain: immunoglobulin homology <IMM>

Query Match 47.5%; Score 276; DB 2; Length 88;
Best Local Similarity 63.2%; Pred. No. 2.1e-20;
Matches 48; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
Qy 23 SRTPETCVVVDVSHEDPVEKFNWYDGVVHNAKTPREEQYNSTYRVVSVLTVLHODW 82
Db 1 SLTPKVTCTVVDVSEDDPDVQISFVNNVEVHTAQOTHRDYNSTIRVVSTLPIQHODW 60
Qy 83 LAGKEYCKVKVSNKGLP 98
Db 61 MSGKEFKCKVNNKDL 76

RESULT 2

I68726 IgE chain C3 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C;Accession: I68726

R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s

A;Reference number: I54443; MUID:88152907; PMID:3346043

A;Accession: I68726

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-107 <RES>

A;Cross-references: GB:M22930; NID:G194455; PIDN:AAA37911.1; PID:G194460

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;22-90/Domain: immunoglobulin homology <IMM>

Db 6 GVITLPPSLD-LYQNGAPKLTCLVVDLSEKKNVNTWQEKTSVSASQWY---TKH 61
Qy 54 HNAKTKPREQYNTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 107
Db 62 HN-----NATTSITSLPVAKDWIBGYGVCIVDHPDFPKPIVRSITK 105

RESULT 5

S26653
Ig kappa chain C region - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S26653
R:Erlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A:Reference number: S26652; MUID:91355693; PMID:2129418
A:Accession: S26653
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-99 <EHR>
A:Cross-references: EMBL:X65287
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 23.1%; Score 134; DB 2; Length 99;
Best Local Similarity 33.3%; Pred. No. 2.7e-06;
Matches 34; Conservative 20; Mismatches 42; Indels 6; Gaps 3;

Qy 4 VAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPR 61

Db 2 VAAPSVEIFP--PSDEQLKSGTASVCLLNNFYPR--EAKYQWKVDNALQSGNSQESVTE 57

Qy 62 EEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEK 103

Db 58 QDSKDSYSLSSLTLSKADYERKHVACEVTHQGLSPVTK 99

RESULT 6

B30554
Ig lambda chain C region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30554
R:Poley, R.C.; Beh, K.J.

J. Immunol. 142, 708-711, 1989

A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.

A:Reference number: A30554; MUID:89093962; PMID:2492052

A:Accession: B30554

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-105 <FOL>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:20-88/Domain: immunoglobulin homology <IMM>

Query Match 23.0%; Score 133.5; DB 2; Length 105;
Best Local Similarity 30.6%; Pred. No. 3.2e-06;
Matches 33; Conservative 22; Mismatches 46; Indels 7; Gaps 4;

Qy 3 PVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61

Db 2 PKSAPSVTLPPPSKEE--LDTNKATVCLISD--FYFGSVNVVWKADGSIINQNVKTQA 57

Qy 62 EEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 109

Db 58 SKQSNKYAASVLTLTGSEWKSSTCEVTHG--STVTKTVKPS 103

RESULT 7

B26167

Ig lambda chain C region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B26167
R:Parvari, R.; Ziv, B.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
A:Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germi
A:Reference number: A26167; MUID:87218480; PMID:3107981
A:Accession: B26167
A:Molecule type: mRNA; DNA
A:Residues: 1-103 <PAR>
A:Cross-references: UNIPROT:P20763; GB:M333049
A:Note: 90-Asp was found in one cDNA clone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-87/Domain: immunoglobulin homology <IMM>

Query Match 22.7%; Score 132; DB 2; Length 103;
Best Local Similarity 29.9%; Pred. No. 4.4e-06;
Matches 32; Conservative 25; Mismatches 44; Indels 6; Gaps 5;

Qy 3 PVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62

Db 2 PKVAPTITLPPPS-KEELNEATKATLVCLINDF-YPPSP-VTVVDVIDG-STRSGETTAQ 57

Qy 63 EQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 109

Db 58 RQSNQYMASSVLSLSGASDSSSHETVTCRVTHNG--TSITKTLKRSE 102

RESULT 8

B26434

Ig lambda-5 chain C region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996

C:Accession: B26434

R:Sakaguchi, N.; Melchers, F.

Nature 324, 579-582, 1986

A:Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lympho

A:Reference number: A26434; MUID:87065143; PMID:3024017

A:Accession: B26434

A:Molecule type: mRNA

A:Residues: 1-105 <SAK>

A:Cross-references: GB:M30387

A:Note: the authors translated the codon TAC for residue 84 as Thr

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 22.6%; Score 131.5; DB 2; Length 105;
Best Local Similarity 32.4%; Pred. No. 5e-06;
Matches 35; Conservative 25; Mismatches 41; Indels 7; Gaps 5;

Qy 3 PVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61

Db 2 PKSDPLVTLPLSLKN-LQPTR-PQLVCLVSE--FPGTLVDVKNVDGVPVQTGVETQP 57

Qy 62 EEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 109

Db 58 SKQTNNKYMVSVYLTLSIDQMPHSRYSCRVTHEG--NTVEKSVSPA 103

RESULT 9

S43147

Ig upsilon chain - duck (fragment)

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000

C:Accession: S43147

R:Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.

submitted to the EMBL Data Library, March 1994

A:Description: Evidence from duck immunoglobulin genes that Igy is the common ancestor o

A:Reference number: S43145

A:Accession: S43147

A:Status: preliminary

RESULT 13

L2HU
Ig lambda chain C regions - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1991 #sequence revision 31-Jan-1981 #text change 09-Jul-2004
C:Accession: A92057; A90243; A91970; A91650; A90375; B90361; A93268; A02125
R/Titan, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A:Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete
A:Reference number: A92057; MUID:70166723; PMID:4909564
A:Contents: Bence Jones protein Sh
A:Accession: A92057
A:Molecule type: protein
A:Residues: 1-105 <TIT>
A:CROSS-references: UNIPROT:P01842
R/Milstein, C.; Clegg, J.B.; Jarvis, J.M.
Biochem. J. 110, 631-652, 1968
A:Title: Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jones
A:Reference number: A90243; MUID:69089380; PMID:4893841
A:Contents: Bence Jones protein X; disulfide bonds
A:Accession: A90243
A:Molecule type: protein
A:Residues: 1-105 <MIL>
R/Kamefani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
A:Title: Comparative studies on the structure of the light chains of human immunoglobulin
A:Reference number: A91970; MUID:83186114; PMID:6404900
A:Contents: Bence-Jones protein Nig-64
A:Accession: A91970
A:Molecule type: protein
A:Residues: 1-105 <KAM>
R/Ponstingl, H.; Hess, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 352, 247-266, 1971
A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom lambda-Typ, Su
A:Reference number: A91650; MUID:71150336; PMID:5549568
A:Contents: Bence Jones protein Kern
A:Accession: A90375
A:Molecule type: protein
A:Residues: 1-44, 'G', 46-105 <PON>
A:Note: this sequence has the Kern+ marker, 45-Gly (instead of Ser)
R/Chen, B.L.; Poljak, R.J.
Biochemistry 13, 1295-1302, 1974
A:Title: Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobul
A:Reference number: A90375; MUID:74109253; PMID:4814727
A:Contents: myeloma protein Newn; partial sequence
A:Accession: A90375
A:Molecule type: protein
A:Residues: 1-81, 'K', 83-105 <CHE>
A:Note: this chain has the Oz+ marker, 82-Lys (instead of Arg)
R/Poljak, R.J.; Amzel, L.M.; Avey, H.P.; Chen, B.L.; Phizackerley, R.P.; Saul, F.
Proc. Natl. Acad. Sci. U.S.A. 71, 3440-3444, 1974
A:Title: The three-dimensional structure of the Fab' fragment of a human myeloma immunog
A:Reference number: A93788; MUID:75046825; PMID:4215080
A:Contents: annotation; Newn; X-ray crystallography, 2.0 angstroms
R/Fett, J.W.; Deutsch, H.F.
Biochemistry 13, 4102-4114, 1974
A:Title: Primary structure of the Mcg lambda chain.
A:Reference number: A90381; MUID:75013804; PMID:4415202
A:Contents: Bence Jones protein Mcg; partial sequence
A:Accession: B90381
A:Molecule type: protein
A:Residues: 1-4, 'N', 6, 'T', 8-44, 'G', 46-55, 'K', 57-105 <FET>
A:Note: this sequence has the Kern+ marker, 45-Gly, and the Mcg+ marker, 5-Asn, 7-Thr, a
R/Edmondson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.
Biochemistry 14, 3953-3961, 1975
A:Title: Rotational allomerism and divergent evolution of domains in immunoglobulin lig
A:Reference number: A90391
A:Contents: annotation; Mcg; X-ray crystallography, 2.3 angstroms
R/Hietter, P.A.; Hollis, G.F.; Korsmeyer, S.J.; Waldmann, T.A.; Leder, P.
Nature 294, 536-540, 1981
A:Title: Clustered arrangement of immunoglobulin lambda constant region genes in man.
A:Reference number: A93268; MUID:82080680; PMID:6273747
A:Accession: A93268

A:Molecule type: DNA
A:Residues: 1-105 <HIE>
A:CROSS-references: GB:J00253; NID:gi86118; PIDN:AAA59107.1; PID:gi86127
A:Note: six tandem lambda-type genes were identified and the three most 5' were sequence
ce (lambda-3)
C:Comment: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins Sh, X, and N
C:Genetics:
A:Gene: GDB:IGLC2; IGLC
A:CROSS-references: GDB:120691; OMIM:147220
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer
F/20-88/Domain: immunoglobulin homology <IMM>
F/27-86/Disulfide bonds: #status experimental
F/104/Disulfide bonds: interchain (to heavy chain) #status experimental
Query Match 20.4%; Score 118.5; DB 1; Length 105;
Best Local Similarity 28.6%; Pred. No. 9.7e-05;
Matches 30; Conservative 23; Mismatches 45; Indels 7; Gaps 4;
QY 3 PVAGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61
DB 2 PKAAPSVTLFPPSSEER--LQANKATLVCLISD--FPGAVTVAAKADSSPKAGVETTP 57
QY 62 EEQYNSTYRVVSVLTVTLQHDWLNKKEYCKVSNKGLPSSIEKTIS 106
DB 58 SKQSNKYAAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTV 100
RESULT 14
H32529
Ig lambda chain C region (clone pDH2) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: H32529
R/Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.
Biochem. J. 245, 691-697, 1987
A:Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length v
A:Reference number: A90338; MUID:88024122; PMID:3117050
A:Accession: H32529
A:Molecule type: mRNA
A:Residues: 1-105 <HAY>
A:CROSS-references: GB:M25620; NID:G294487; PIDN:AAA5092.1; PID:G561834
A:Note: the authors translated the codon GTC for residue 84 as Thr and ACC for residue 8
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/20-88/Domain: immunoglobulin homology <IMM>
Query Match 20.4%; Score 118.5; DB 2; Length 105;
Best Local Similarity 28.7%; Pred. No. 9.7e-05;
Matches 31; Conservative 21; Mismatches 49; Indels 7; Gaps 4;
QY 3 PVAGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
DB 2 PAVTPSVILFPPSSEER--LKDNKATLVCLIND--FYPGTVKVWKAKDGTPTQGVDTQP 57
QY 62 EEQYNSTYRVVSVLTVTLQHDWLNKKEYCKVSNKGLPSSIEKTISKAK 109
DB 58 SKQSNKYAAASSFLSLSANQWKSYQSVTCVTHEG--HTVEKSLAPAE 103
RESULT 15
S26654
Ig lambda chain C region - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S26654
R/Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A:Reference number: S26652; MUID:91355693; PMID:2129418

A;Accession: S26654
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-98 <EHR>
A;Cross-references: EMBL:X65286
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-88/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 117.5; DB 2; Length 98;
Best Local Similarity 30.1%; Pred. No. 0.00011;
Matches 31; Conservative 20; Mismatches 45; Indels 7; Gaps 4;
QY 3 PVAGPSVFLFPPPKDITLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61
Db | | | | | | | | | | : : : : : | | | | | : |
QY 2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYPGAVTVAWKADSSFPKAGVETTP 57
Db : | | | | | | | | | | : : : : : | | | | | : |
QY 62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKT 104
Db : | | | | | | | | | | : : : : : | | | | | : |
Db 58 SKQSNKNYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKT 98

Search completed: November 17, 2005, 07:55:07
Job time : 17.4247 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.1461 Seconds
(without alignments)
723.518 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVFLPPPKPKDTL.....CKVSNKGLPSSIEKTIKAK 109

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	139	23.9	106	1	KAC_HUMAN	P01834 homo sapien
2	132	22.7	103	1	LAC_CHICK	P20763 gallus gall
3	127.5	21.9	105	1	LAC1_MOUSE	P01843 mus musculus
4	126.5	21.8	105	1	LAC5_MUSSP	P20765 mus spratus
5	122.5	21.1	105	1	LAC5_MOUSE	P20764 mus musculus
6	121.5	20.9	106	2	O8TCJ5	O8TCJ5 homo sapien
7	118.5	20.4	105	1	LAC_HUMAN	P01842 homo sapien
8	113.5	19.5	105	1	LAC_RABIT	P01847 oryctolagus
9	112.5	19.4	103	1	KAC4_RABIT	P01840 oryctolagus
10	108.5	18.7	105	1	LAC_PIG	P01846 sus scrofa
11	108	18.6	104	1	LAC1_RAT	P20766 rattus norv
12	107	18.4	106	1	KAC_MOUSE	P01837 mus musculus
13	104	17.9	104	1	KAC5_RABIT	P03984 oryctolagus
14	99	17.0	104	1	LAC2_RAT	P20767 rattus norv
15	99	17.0	106	1	KACB_RABIT	P01839 oryctolagus
16	99	17.0	106	1	KACB_RAT	P01835 rattus norv
17	94	16.2	104	1	LAC3_MOUSE	P01845 mus musculus
18	94	16.2	106	1	KAC3_RAT	P01836 rattus norv
19	93	16.0	104	1	KAC5_RABIT	P01838 oryctolagus
20	92	15.8	103	1	KAC5_RABIT	P01841 oryctolagus
21	80	13.8	104	1	LAC2_MOUSE	P01844 mus musculus
22	80	13.8	105	2	O99JC1	O99JC1 mus musculus
23	66	11.4	107	2	O8KVI0	O8KVI0 bacillus an
24	65	11.4	107	2	O6E2I5	O6E2I5 bacillus an
25	63	10.8	98	2	O7XZF9	O7XZF9 oryza sativ
26	62	10.7	93	2	O6LBNV	O6LBNV mus musculus
27	61.5	10.6	93	2	O6LBN2	O6LBN2 mus musculus
28	61	10.5	91	2	O9JKP1	O9JKP1 marmota mon
29	60.5	10.4	74	2	P79659	P79659 oncorhynch
30	60.5	10.4	74	2	P79660	P79660 oncorhynch
31	60	10.3	73	2	O8FBY4	O8FBY4 escherichia

32	59	10.2	79	1	SNSP_HUMAN	P80697 homo sapien
33	59	10.2	91	2	Q31248	Q31248 peromyscus
34	59	10.2	93	2	Q31158	Q31158 mus musculus
35	58.5	10.1	55	2	Q768W8	Q768W8 uncultured
36	58.5	10.1	93	2	O19471	O19471 mus musculus
37	58.5	10.1	93	2	O19472	O19472 mus musculus
38	58.5	10.1	93	2	Q9QUH8	Q9QUH8 mus musculus
39	58	10.0	103	2	Q8HX76	Q8HX76 sus scrofa
40	58	10.0	104	2	Q8C5T6	Q8C5T6 mus musculus
41	58	10.0	106	2	Q31261	Q31261 rattus norv
42	57.5	9.9	55	2	Q768W5	Q768W5 uncultured
43	57.5	9.9	65	1	DN71_SULAC	P13123 sulfolobus
44	57.5	9.9	95	1	DAFT_TRYCR	Q26327 trypanosoma
45	57	9.8	90	1	ALB2_SULTO	Q97116 sulfolobus

ALIGNMENTS

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Ig kappa chain C region.			
GN	Name=IGKC;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU)			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=49231144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;			
RA	Hietar P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,			
RT	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(in) Franek F., Shugar D. (eds.);			
RL	Gamma Globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM)			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).

RN [7]

RP SEQUENCE (BENCE-JONES PROTEIN AG).

RX MEDLINE=69234734; PubMed=4893682;

RA Titani K., Shinoda T., Putnam F.W.;

RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";

RL J. Biol. Chem. 244:3550-3560(1969).

RN [8]

RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).

RX MEDLINE=70201507; PubMed=5447531;

RA Kohler H., Shimizu A., Paul C., Putnam F.W.;

RT "Macroglobulin structure: variable sequence of light and heavy chains.";

RL Science 169:56-59(1970).

RN [9]

RP SEQUENCE OF 1-33; 38-41 AND 62-80.

RC TISSUE=Abdominal adipose tissue;

RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;

RA Olsen K.E., Sletten K., Westermarck P.;

RT "Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";

RL Biochem. Biophys. Res. Commun. 245:713-716(1998).

CC -1- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker, Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic marker, Ala-45 and Leu-83.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -----

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CC -----

DR EMBL; J00241; AAA58989.1; -.

DR PIR; B90562; K3HU.

DR PDB; 1DSB; X-ray; A/L=1-103.

DR PDB; 1DS1; X-ray; L=1-103.

DR PDB; 1D6V; X-ray; L=1-103.

DR PDB; 1HEZ; X-ray; -.

DR PDB; 1HKL; X-ray; L=1-106.

DR PDB; 1I7Z; X-ray; A/C=1-106.

DR PDB; 1MIM; X-ray; L=1-105.

DR PDB; 1MIM; X-ray; L=1-105.

DR H-InvDB; HIX0021121; -.

DR MIM; 147200; -.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR PROSITE; PS50835; IG LIKE; 1.

DR PROSITE; PS00290; IG_MHC; 1.

KW 3D-structure: Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.

KW NON_TER 1 1

FT DOMAIN 5 102 Ig-like.

FT DISULFID 26 86

FT VARIANT 106 106 Interchain (with a heavy chain).

FT V -> L (in INV(1,2) marker).

FT /FTID=VAR_003897.

FT D -> N (in Ref. 7 and 8).

FT E -> Q (in Ref. 5 and 6).

FT CONFLICT 14 14

FT CONFLICT 57 57

FT STRAND 3 3

FT STRAND 6 10

FT HELIX 14 17

FT TURN 18 20

FT TURN 21 32

FT STRAND 37 42

FT TURN 43 44

FT STRAND 45 47

FT STRAND 51 55

FT TURN 60 62

FT STRAND 65 74

FT HELIX 75 79

FT TURN 80 80

FT STRAND 83 89

FT TURN 91 92

FT STRAND 97 102

FT TURN 103 104

SQ SEQUENCE 106 AA; 51984D1PDD372CE8 CRC64;

Query Match 23.9%; Score 139; DB 1; Length 106;

Best Local Similarity 31.5%; Pred.No. 6.2e-06;

Matches 34; Conservative 24; Mismatches 44; Indels 6; Gaps 3;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG--EVFNAKTKPR 61

DB 2 VAAPSVFIFP--PSDQLKSGTASVCLLNFFYPR--EAKVQWKVDNALQSGNSQESVTE 57

QY 62 BEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109

DB 58 QDSKSTYSLSSTLTLSKADYKKHYACEVTHQGLSSPVTKSFNRGE 105

RESULT 2

LAC_CHICK

ID LAC_CHICK STANDARD; PRT; 103 AA.

AC P20763;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig lambda chain C region.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87218480; PubMed=3107981;

RA Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;

RT "Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus.";

RL EMBO J. 6:97-102(1987).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -----

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CC -----

DR EMBL; X04768; CAA28461.1; -.

DR PIR; B26167; B26167.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00407; Igc1; 1.

DR PROSITE; PS50835; IG LIKE; 1.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin C region; Immunoglobulin domain; Polymorphism.

KW NON_TER 1 1

FT DOMAIN 6 99 Ig-like.

FT DISULFID 28 85

FT DISULFID 103 103 Interchain (with heavy chain).

FT VARIANT 90 90 N -> D.

SQ SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;

Query Match 22.7%; Score 132; DB 1; Length 103;
 Best Local Similarity 29.9%; Pred. No. 2.9e-05;
 Matches 32; Conservative 25; Mismatches 44; Indels 6; Gaps 5;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
 DB 2 PKVAPTTILPPPS-KEELNEATKATLVCLINDF-YPSF-VTVVDVWG-STRGETTAPQ 57

QY 63 EQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
 DB 58 RQNSQYMASSYLSASDWSHETTCRVTHNG-TSITKTKRSE 102

RESULT 3
 LAC1 MOUSE STANDARD; PRT; 105 AA.

AC P01843;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig lambda-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83014953; PubMed=6812053;
 RA Selsing E., Miller J., Wilson R., Storb U.;
 RT "Evolution of mouse immunoglobulin lambda genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685 (1982).
 RN [2]
 RP SEQUENCE FROM N.A. (MOPC 315).
 RX MEDLINE=81148806; PubMed=6259534;
 RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
 RA Gafter M.B., Baltimore D.;
 RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
 RL Nature 290:65-67 (1981).
 RN [3]
 RP SEQUENCE FROM N.A. (S43).
 RX MEDLINE=82220143; PubMed=6283385;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Somatic variants of murine immunoglobulin lambda light chains.";
 RL Nature 298:380-382 (1982).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
 RX MEDLINE=71107854; PubMed=5276767;
 RA Appella E.;
 RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594 (1971).
 CC -1- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
 normal lambda-2 chain and 1 abnormal lambda-1 chain that is
 missing a large part of the V region. The C region sequence (shown
 here) appears completely normal.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC
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 CC
 CC EMBL; J00582; AAAS1636.1; -;
 CC EMBL; J00587; AABS9672.1; -;
 CC PIR; A93922; LIMS.
 CC PDB; 1JNH; X-ray; A=1-105.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 1.

DR PROSITE; PS50835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
 KW Immunoglobulin domain.
 FT NON_TER 1 100 Ig-like.
 FT DOMAIN 6 100
 FT DISULFID 27 86
 FT DISULFID 104 104
 FT CONFLICT 19 20 Interchain (with heavy chain).
 FT CONFLICT 56 56 ET -> TE (in Ref. 4).
 FT CONFLICT 75 75 Q -> E (in Ref. 4).
 FT CONFLICT 81 82 Missing (in Ref. 4).
 FT CONFLICT 85 85 HS -> SH (in Ref. 4).
 FT CONFLICT 96 96 S -> SS (in Ref. 4).
 FT CONFLICT 96 96 E -> Q (in Ref. 4).
 FT STRAND 4 4
 FT STRAND 7 7
 FT STRAND 10 11
 FT STRAND 15 19
 FT TURN 20 21
 FT STRAND 22 33
 FT STRAND 37 43
 FT TURN 44 45
 FT STRAND 46 48
 FT TURN 50 51
 FT STRAND 52 54
 FT STRAND 58 60
 FT TURN 61 63
 FT STRAND 64 74
 FT HELIX 75 80
 FT STRAND 84 90
 FT TURN 91 92
 FT STRAND 93 99
 SQ SEQUENCE 105 AA; A89F2B09BCFCA018 CRC64;

Query Match 21.9%; Score 127.5; DB 1; Length 105;
 Best Local Similarity 30.8%; Pred. No. 8.3e-05;
 Matches 33; Conservative 19; Mismatches 48; Indels 7; Gaps 3;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
 DB 2 PKSSPSVTLFPPPSSEEL---ETNKATLVCTITDFYPGVTVVDKVDGTPVTQGMETTP 57

QY 62 EQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 108
 DB 58 SKQSNKNYMASSYLSLTARAWERHSHSYSCQVTHEG--HTVEKSLSR 102

RESULT 4
 LAC5 MUSSP STANDARD; PRT; 105 AA.

AC P20765;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda-5 chain C region.
 OS Mus spretus (Western wild mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88196070; PubMed=3129289;
 RA Mami F., Cazenave P.A., Kindt T.J.;
 RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
 RL EMBO J. 7:117-122 (1988).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J00582; AAAS1636.1; -;
 CC EMBL; J00587; AABS9672.1; -;
 CC PIR; A93922; LIMS.
 CC PDB; 1JNH; X-ray; A=1-105.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 1.

GN and Name=IGLC2;
GN and
GN Name=IGLC3;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN SH).
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges.";
RL J. Biol. Chem. 245:2171-2176(1970).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX MEDLINE=6908380; PubMed=4883841;
RA Milstein C., Clegg J.B., Jarvis J.M.;
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT Bence-Jones protein.";
RL Biochem. J. 110:631-652(1968).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup.";
RL J. Biochem. 93:421-429(1983).
RN [4]
RP SEQUENCE (BENCE-JONES PROTEIN KERN).
RX MEDLINE=71150336; PubMed=5549568;
RA Ponstingl H., Hess M., Hilschmann N.;
RT "Structural rule of antibodies. Primary structure of a monoclonal
RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT protein Kern). V. The complete amino acid sequence and its genetic
RT interpretation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN [5]
RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX MEDLINE=74109253; PubMed=4814727;
RA Chen B.L., Poljak R.J.;
RT "Amino acid sequence of the (lambda) light chain of a human myeloma
RT immunoglobulin (IGG New).";
RL Biochemistry 13:1295-1302(1974).
RN [6]
RP SEQUENCE (DOT).
RX MEDLINE=9525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavon monoclinal
RT immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX MEDLINE=75046825; PubMed=4215080;
RA Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA Saul F.;
RT "The three-dimensional structure of the fab' fragment of a human
RT myeloma immunoglobulin at 2.0-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN [8]
RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX MEDLINE=75013804; PubMed=4415202;
RA Felt J.W., Deutch H.F.;
RT "Primary structure of the Mcg lambda chain.";
RL Biochemistry 13:4102-4114(1974).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RA Edmondson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
RT immunoglobulin light chains.";
RL Biochemistry 14:3953-3961(1975).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmondson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms.";
RL J. Mol. Biol. 210:601-615(1989).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=82080680; PubMed=6273747;
RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT "Clustered arrangement of immunoglobulin lambda constant region genes
RT in man.";
RL Nature 294:536-540(1981).
RN [12]
RP MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain
CC found in proteins SH, X, and NIG-64. The Kern protein has the
CC Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein
CC has the Kern+ marker, and the Mcg+ marker.
CC -1- MISCELLANEOUS: Six tandem lambda-type genes were identified and
CC the 3 most 5' were sequenced. These correspond to the Mcg sequence
CC (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+
CC sequence (lambda-3).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL: J00253; AAA59107.1; -
DR EMBL: L38562; AAB36581.1; ALT_INIT.
DR EMBL: X51754; CAB38569.1; ALT_INIT.
DR EMBL: X51755; CAA36049.1; -
DR EMBL: X51755; CAA36051.1; -
DR PIR: A92057; L2HU.
DR PDB: 1AOK; X-ray; L=1-105.
DR PDB: 1LIL; X-ray; A/B=1-105.
DR PDB: 2MCG; X-ray; -
DR PDB: 7FAB; X-ray; L=1-105.
DR Genew; HGNC:5855; IGLC1.
DR Genew; HGNC:5856; IGLC2.
DR Genew; HGNC:5857; IGLC3.
DR H-InvDB; HIX0016285; -
DR MIM: 147220; -
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig, 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86 Interchain (with heavy chain).
FT DISULFID 104 104 A -> N (in MCG+ marker).
FT VARIANT 5 5 /FTId=VAR_003898.
FT VARIANT 7 7 S -> T (in MCG+ marker).
FT VARIANT 45 45 /FTId=VAR_003899.
FT VARIANT 56 56 /FTId=VAR_003900.
FT VARIANT 82 82 T -> K (in MCG+ marker).
FT VARIANT 82 82 /FTId=VAR_003901.
FT STRAND 8 11 R -> K (in OZ+ marker).
FT /FTId=VAR_003902.

```
FT HELIX 15 19
FT TURN 20 21
FT STRAND 24 32
FT STRAND 38 43
FT TURN 44 45
FT STRAND 46 48
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 72
FT HELIX 75 80
FT STRAND 84 89
FT STRAND 94 99
SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match 20.4%; Score 118.5; DB 1; Length 105;
Best Local Similarity 28.6%; Pred. No. 0.00064;
Matches 30; Conservative 23; Mismatches 45; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61
DB 2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYPGAVTVAMKADSSPVKAGVETTP 57

QY 62 EEQYNSTYRVVSVLTVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIIS 106
DB 58 SKQSNKNKYAASSYLSTLTPPEQWKSHRSYQCVTHG--STVEKTV 100

RESULT 8
LAC_RABIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE
RX MEDLINE=82091105; PubMed=6797414;
RA Garcia I., Jaton J.-C.;
RT "The primary structure of the constant region of Basilea-rabbit
RT immunoglobulin lambda-chains.";
RL Biochem. J. 197; 177-183 (1981).
CC -I- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
CC specificity.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02130; L7RB.
DR HSSP; P01842; 1AQK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 19.5%; Score 113.5; DB 1; Length 105;
Best Local Similarity 27.8%; Pred. No. 0.002;
Matches 30; Conservative 21; Mismatches 50; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
DB 2 PAVTPSVILFPPSSEE--LKDKNATLVCLISDFYPR--TVKNWVKADGNSVTGGVDITQP 57
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QY 62 EEQYNSTYRVVSVLTVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISAK 109
DB 58 SKQSNKNKYAASSFLHLTANQWKSYQSVTCQVTHG--HTVEKSLAPAE 103

RESULT 9
KAC4_RABIT STANDARD; PRT; 103 AA.
ID KAC4_RABIT
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6412231;
RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT allotype J-C locus and evidence for several b4-related sequences in
RT the rabbit genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713 (1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806 (1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S., Kindt T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
RT to streptococcal carbohydrate. II. Sequence determination of peptides
RT from tryptic and peptic digests.";
RL J. Biol. Chem. 250:3289-3296 (1975).
CC -I- MISCELLANEOUS: This chain was obtained from antibody to the
CC specific carbohydrate of group C Streptococci and was isolated
CC from the serum of a single rabbit.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).
DR EMBL; X00231; CAA25051.1; -.
DR PIR; A93971; K4RB.
DR HSSP; P01837; 1KCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 5 95 Ig-like.
FT DISULFID 26 85
FT DISULFID 103 103 Interchain (with a heavy chain).
FT CONFLICT 58 58 N -> D (in Ref. 3).
SQ SEQUENCE 103 AA; 11043 MW; 5FC5ACC8B60E68DB CRC64;

Query Match 19.4%; Score 112.5; DB 1; Length 103;
Best Local Similarity 31.7%; Pred. No. 0.0024;
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Matches 33; Conservative 19; Mismatches 39; Indels 13; Gaps 6;
Oy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE----VHNAKT 58
Db 2 PVA-PTVLIFPPAADQ--VATGTVIVCV---ANKYFPDVTVTWEVDGTTTGTGIESKT 55
Oy 59 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE 102
Db 56 P--QNSADCTYNLSSTLTSTQNSHKYCKVT-QGTTSVWQ 96

RESULT 10
LAC_PIG
ID LAC_PIG STANDARD; PRT; 105 AA.
AC P01846;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
PP SEQUENCE.
RX MEDLINE=7800254; PubMed=409425;
RA Novotny J., Franek F., Margolies M.N., Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
immunoglobulin lambda chains.";
RL Biochemistry 16:3765-3772(1977).
CC -1- MISCELLANEOUS: This chain was obtained from a mixture of normal
immunoglobulins.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02129; L1PG.
DR HSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 2 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match 18.7%; Score 108.5; DB 1; Length 105;
Best Local Similarity 28.4%; Pred. No. 0.0061;
Matches 31; Conservative 20; Mismatches 49; Indels 9; Gaps 4;
Oy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA--KTKP 60
Db 2 PKAAPTNLPPPSSEEL----GINKATLVCLISDFYPCGAVTVTWKAGGTTVTOGVETKTP 57
Oy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 58 -SKQSNKYAASSYLALSADWKSSTSGTTCQVTHEG--TIVEKTVTPSE 103

RESULT 11
LAC1_RAT
ID LAC1_RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01843; 1JNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
FT DISULFID 104 104
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC878A CRC64;

Query Match 18.6%; Score 108; DB 1; Length 104;
Best Local Similarity 25.2%; Pred. No. 0.0068;
Matches 27; Conservative 23; Mismatches 51; Indels 6; Gaps 2;
Oy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE 62
Db 2 PKATPSVTLFPPSSEEL---KTDKATLVCMVTDYFGVMTVMWKADGTPITQGVETTP 57
Oy 63 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 58 FKQNNKYMATSYLLLTAKAWETHSNYSQVTHE--ENTVEKSLRAE 102

RESULT 12
KAC_MOUSE
ID KAC_MOUSE STANDARD; PRT; 106 AA.
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
PP SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
RN [3]
```



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CC -----
DR EMBL; X00032; -; NOT_ANNOTATED_CDS.
DR PIR; A01363; AAA31355.1; -.
DR HSP; P01837; K5RBV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT DOMAIN 1 1 Ig-like.
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
FT CONFLICT 1 1 A -> VA (in Ref. 2)
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 17.9%; Score 104; DB 1; Length 104;
Best Local Similarity 26.7%; Pred. No. 0.017;
Matches 28; Conservative 24; Mismatches 41; Indels 12; Gaps 5;

Qy 7 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG-----VEVHNAKTKPRE 62
Db 5 PTVLIFPPSPAE--LATGATIVCV---ANKYFPDGTVTWQVDGKPLTTGIETSKTPQNS 59

Qy 63 EQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTSK 107
Db 60 D--CTYLSSTLTLSKDEYNHDEYTCQVA-QGSGSPVQVQFSR 101

RESULT 14
LAC2 RAT STANDARD; PRT; 104 AA.
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-2 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
RL and a single V lambda gene."
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; M22521; AAA41420.1; ALT_INIT.
CC HSP; P01842; 2MCG.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; IGC1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT DOMAIN 1 1
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 17.9%; Score 104; DB 1; Length 104;
Best Local Similarity 26.7%; Pred. No. 0.017;
Matches 28; Conservative 24; Mismatches 41; Indels 12; Gaps 5;

Qy 7 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG-----VEVHNAKTKPRE 62
Db 5 PTVLIFPPSPAE--LATGATIVCV---ANKYFPDGTVTWQVDGKPLTTGIETSKTPQNS 59

Qy 63 EQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTSK 107
Db 60 D--CTYLSSTLTLSKDEYNHDEYTCQVA-QGSGSPVQVQFSR 101

RESULT 14
LAC2 RAT STANDARD; PRT; 104 AA.
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-2 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
RL and a single V lambda gene."
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
CC EMBL; M22521; AAA41420.1; ALT_INIT.
CC HSP; P01842; 2MCG.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; IGC1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT DOMAIN 1 1
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 17.0%; Score 99; DB 1; Length 104;
Best Local Similarity 21.5%; Pred. No. 0.052;
Matches 23; Conservative 28; Mismatches 50; Indels 6; Gaps 3;

Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
Db 2 PKSTPTLTVPFPSTES--LQGNKATLVCLISDYPSDVEVA--WKANGAPISQGVDTANP 57

Qy 63 EQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTSK 109
Db 58 TKQGNKYIASSFLRLTAEQWRSRNSFTQVTHEG--NTVEKSLSPAE 102

RESULT 15
KACB RABIT STANDARD; PRT; 106 AA.
AC P01839;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa-b4 chain C region.
GN Names=K-BAS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Basilea;
RX PubMed=11894960;
RA Heidmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit
RL genome: a b4b4 homozygous rabbit contains a kappa-bas gene."
RL EMBO J. 2:437-441(1983).
CC -1- MISCELLANEOUS: In Basilea rabbits, the major type of light chain
CC is lambda. The kappa chain shown is a minor component. All other
CC rabbit B allotypes have Cys-64.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
CC EMBL; V01241; CAA24558.1; -.
CC EMBL; V00885; -; NOT_ANNOTATED_CDS.
CC PIR; A02121; K4RBBS.
CC HSP; P01837; 25C8.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT DOMAIN 1 1
FT DISULFID 27 87
FT DISULFID 106 106 Interchain (with a heavy chain).
SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 17.0%; Score 99; DB 1; Length 106;
Best Local Similarity 29.4%; Pred. No. 0.053;
Matches 32; Conservative 21; Mismatches 44; Indels 12; Gaps 6;

Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE-----VHNAKT 58

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.3927 Seconds
(without alignments)
347.833 Million cell updates/sec

Title: US-09-674-857-1
Perfect score: 581
Sequence: 1 APPVAGPSVFLPPKPKDTL.....CKVSNKGLPSSIBXTISKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	95.4	109	3	US-08-444-644-30
2	554	95.4	109	3	US-08-232-246A-30
3	542	93.3	110	3	US-08-444-644-21
4	542	93.3	110	3	US-08-232-246A-21
5	541	93.1	105	2	US-08-232-539D-60
6	540	92.9	109	2	US-08-070-116A-4
7	540	92.9	109	4	US-08-557-050-4
8	540	92.9	110	3	US-08-444-644-44
9	540	92.9	110	3	US-08-232-246A-44
10	518	89.2	110	3	US-08-444-644-38
11	518	89.2	110	3	US-08-232-246A-38
12	329	56.6	66	3	US-08-569-147-85
13	175	30.1	107	4	US-09-281-760B-36
14	166.5	28.7	106	2	US-08-232-539D-54
15	152	26.2	109	3	US-08-466-163B-1
16	152	26.2	109	4	US-09-802-096-1
17	152	26.2	109	4	US-09-802-077-1
18	141	24.3	100	1	US-08-422-101-10
19	141	24.3	100	1	US-08-422-091-10
20	141	24.3	100	2	US-08-422-092-10
21	141	24.3	100	2	US-08-788-800-7
22	141	24.3	100	3	US-08-422-093-10
23	141	24.3	100	3	US-08-422-112-10
24	139	23.9	105	3	US-09-025-769B-166
25	139	23.9	105	4	US-09-490-070A-166
26	139	23.9	105	4	US-09-490-153-166
27	139	23.9	105	4	US-09-490-324-166

28 139 23.9 106 2 US-08-378-939-40 Sequence 40, Appl
29 139 23.9 106 2 US-08-761-277A-49 Sequence 49, Appl
30 139 23.9 106 3 US-08-444-644-26 Sequence 26, Appl
31 139 23.9 106 3 US-08-232-246A-26 Sequence 26, Appl
32 139 23.9 107 1 US-08-422-101-8 Sequence 8, Appl
33 139 23.9 107 1 US-08-422-091-8 Sequence 8, Appl
34 139 23.9 107 2 US-08-422-092-8 Sequence 5, Appl
35 139 23.9 107 2 US-08-788-800-5 Sequence 5, Appl
36 139 23.9 107 3 US-08-422-093-8 Sequence 8, Appl
37 139 23.9 107 3 US-08-422-112-8 Sequence 8, Appl
38 139 23.9 107 4 US-09-301-593-20 Sequence 20, Appl
39 139 23.9 108 4 US-09-313-942-13 Sequence 13, Appl
40 135 23.2 106 2 US-08-378-939-42 Sequence 42, Appl
41 133.5 23.0 109 2 US-08-646-981-6 Sequence 6, Appl
42 130 22.4 109 1 US-08-436-463-8 Sequence 8, Appl
43 130 22.4 109 1 US-08-024-253-8 Sequence 8, Appl
44 129 22.2 106 1 US-08-399-106A-7 Sequence 7, Appl
45 129 22.2 106 1 US-08-433-105A-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-444-644-30

Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 61 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109

RESULT 2

US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458

FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA: PCT/US90/05077

FILING DATE: 07-SEP-1990
APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:

NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480

REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: internal
US-08-232-246A-30

Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

Db 1 APPVAGSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 61 REEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109

RESULT 3

US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:

APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,644
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458

FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA: PCT/US90/05077

FILING DATE: 07-SEP-1990
APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:

NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480

REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: internal
US-08-444-644-21

Query Match 93.3%; Score 542; DB 3; Length 110;
Best Local Similarity 95.3%; Pred. No. 5.9e-55;
Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 63
Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 64

QY 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109

Db 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 4
 US-08-232-246A-21
 ; Sequence 21, Application US/08232246A
 ; Patent No. 6329508
 ; GENERAL INFORMATION:
 ; APPLICANT: Eriden, Phillip M.
 ; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
 ; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
 ; TITLE OF INVENTION: CONJUGATES
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Millitia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,246A
 ; FILING DATE: 04-MAY-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/800,458
 ; FILING DATE: 26-NOV-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US90/05077
 ; FILING DATE: 07-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/404,089
 ; FILING DATE: 07-SEP-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wagner, Richard W.
 ; REGISTRATION NUMBER: 34,480
 ; REFERENCE/DOCKET NUMBER: ALK88-15AAA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 110 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-232-246A-21

Query Match 93.3%; Score 542; DB 3; Length 110;
 Best Local Similarity 95.3%; Pred. No. 5.9e-55;
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 VAGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
 Db : |||||
 Db 5 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
 Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 Db : |||||
 Db 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 5
 US-08-232-539D-60
 ; Sequence 60, Application US/08232539D
 ; Patent No. 5965709
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; APPLICANT: Jardieu, Paula M.

; TITLE OF INVENTION: IgE Antagonists
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,539D
 ; FILING DATE: 21-Apr-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/178583
 ; FILING DATE: 07-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/744768
 ; FILING DATE: 14-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P0718P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 60:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 105 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-232-539D-60

Query Match 93.1%; Score 541; DB 2; Length 105;
 Best Local Similarity 97.1%; Pred. No. 7.2e-55;
 Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
 Db : |||||
 Db 1 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 60
 Qy 66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 Db : |||||
 Db 61 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 104

RESULT 6
 US-08-070-116A-4
 ; Sequence 4, Application US/08070116A
 ; Patent No. 5885573
 ; GENERAL INFORMATION:
 ; APPLICANT: Zivin, Robert A.
 ; APPLICANT: Jolliffe, Linda K.
 ; APPLICANT: Bluestone, Jeffrey A.
 ; TITLE OF INVENTION: Methods and Materials For Modulation
 ; TITLE OF INVENTION: of the Immuno-suppressive Activity and
 ; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/070,116A
/ FILING DATE: 01-JUN-1993
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: ARCD:082
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 109 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-070-116A-4

Query Match          92.9%; Score 540; DB 2; Length 109;
Best Local Similarity 95.3%; Pred. No. 9.9e-55;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63

Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 7
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; APPLICATION NUMBER: US/08/557,050
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
```

```
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 109 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-557-050-4

Query Match          92.9%; Score 540; DB 4; Length 109;
Best Local Similarity 95.3%; Pred. No. 9.9e-55;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63

Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 8
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALX88-15AAA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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```
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-44

Query Match
Best Local Similarity 92.9%; Score 540; DB 3; Length 110;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
;

RESULT 9
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-44

Query Match
Best Local Similarity 92.9%; Score 540; DB 3; Length 110;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
;

RESULT 10
US-08-444-644-38
; Sequence 38, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-38

Query Match
Best Local Similarity 89.2%; Score 518; DB 3; Length 110;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
;
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RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/082322246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match      89.2%; Score 518; DB 3; Length 110;
Best Local Similarity 91.5%; Pred. No. 3.5e-52;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
; : |||||
Db      5 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKLREE 64
; : |||||

QY      64 QYNSTYRVVSVLTVTLQHDWLNQKEYKCKVSNKGLPSSIEKTISKAK 109
; : |||||
Db      65 QYNSTFRVSVLTVTLQHDWLNQKEYKCKVSNKALPAPIEKTISKAK 110
; : |||||

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
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```
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377rie, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match      56.6%; Score 329; DB 3; Length 66;
Best Local Similarity 96.8%; Pred. No. 1.2e-30;
Matches 60; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
; : |||||
Db      5 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVFNWYVDGVEVHNAKTKPREE 64
; : |||||

QY      64 QY 65
; : ||
Db      65 QY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (413)..(414) stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-36

Query Match 30.1%; Score 175; DB 4; Length 107;
Best Local Similarity 35.0%; Pred. No. 1.3e-12;
Matches 36; Conservative 23; Mismatches 42; Indels 2; Gaps 2;
QY 6 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
DB 5 GVSLSLPPSPFLD-LYVHKAPKTKCLVDLATWE-GNLTWYRESKEPVNPVPLNKDHF 62
QY 66 NSTRYVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIK 108
DB 63 NGTITVTSTLPVNTDWEGETYTCRVTHPHLPKDIVRSIAKA 105

RESULT 14
US-08-232-539D-54
Sequence 54, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Ige Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-54

Query Match 28.7%; Score 166.5; DB 2; Length 106;
Best Local Similarity 34.3%; Pred. No. 1.3e-11;
Matches 35; Conservative 22; Mismatches 44; Indels 1; Gaps 1;
QY 6 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
DB 1 GVSAYLSRSPSPFD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRTRKEKQR 59
QY 66 NSTRYVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIK 107
DB 60 NGTLTSTLPVGTDRDWEGETYTCRVTHPHLPALMRSTTK 101

RESULT 15
US-08-466-163B-1
Sequence 1, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 1
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-08-466-163B-1

Query Match 26.2%; Score 152; DB 3; Length 109;
Best Local Similarity 34.3%; Pred. No. 6.2e-10;
Matches 35; Conservative 21; Mismatches 44; Indels 2; Gaps 2;
QY 6 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
DB 6 GVSAYLSRSPSPFD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRTRKEKQR 64
QY 66 NSTRYVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIK 107

Db 65 NGTLTVTSTLPVGTDRWIEG-ETQCRVTHPHLPRALMRSTTK 105
Search completed: November 17, 2005, 07:53:55
Job time : 24.3927 secs

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 82.3721 Seconds
(without alignments)
553.666 Million cell updates/sec

Title: US-09-674-857-1
Perfect score: 581
Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTSKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US10I_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	98.6	109	18	US-10-959-318-11
2	573	98.6	109	18	US-10-959-318-12
3	562.5	96.8	110	18	US-10-959-318-9
4	562.5	96.8	110	18	US-10-959-318-10
5	559	96.2	109	18	US-10-959-318-15
6	559	96.2	109	18	US-10-959-318-16
7	554	95.4	109	18	US-10-959-318-2
8	548.5	94.4	110	18	US-10-959-318-13
9	548.5	94.4	110	18	US-10-959-318-14
10	548	94.3	110	18	US-10-959-318-7
11	548	94.3	110	18	US-10-959-318-8

12	547	94.1	109	18	US-10-627-556-270	Sequence 270, App
13	546	94.0	109	18	US-10-959-318-17	Sequence 17, Appl
14	546	94.0	109	18	US-10-959-318-18	Sequence 18, Appl
15	544.5	93.7	110	20	US-11-018-102-23	Sequence 23, Appl
16	542.5	93.4	110	20	US-11-018-102-25	Sequence 25, Appl
17	542	93.3	109	14	US-10-207-655-220	Sequence 220, App
18	542	93.3	109	18	US-10-627-556-14	Sequence 14, Appl
19	542	93.3	110	15	US-10-370-749-23	Sequence 23, Appl
20	542	93.3	110	18	US-10-959-318-1	Sequence 1, Appl
21	542	93.3	110	20	US-11-018-102-22	Sequence 22, Appl
22	540	92.9	109	14	US-10-267-286A-4	Sequence 4, Appl
23	540	92.9	110	18	US-10-959-318-4	Sequence 4, Appl
24	540	92.9	110	18	US-10-959-318-21	Sequence 21, Appl
25	540	92.9	110	20	US-11-018-102-24	Sequence 24, Appl
26	538	92.6	109	18	US-10-627-556-294	Sequence 294, App
27	537	92.4	109	14	US-10-020-354-80	Sequence 80, Appl
28	537	92.4	109	18	US-10-627-556-258	Sequence 258, App
29	537	92.4	109	18	US-10-627-556-278	Sequence 278, App
30	537	92.4	109	18	US-10-627-556-302	Sequence 302, App
31	537	92.4	110	15	US-10-370-749-53	Sequence 53, Appl
32	535	92.1	110	18	US-10-959-318-22	Sequence 22, Appl
33	535	92.1	110	18	US-10-959-318-22	Sequence 22, Appl
34	534	91.9	109	14	US-10-207-655-322	Sequence 322, App
35	534	91.9	109	18	US-10-627-556-92	Sequence 92, Appl
36	534	91.9	110	18	US-10-959-318-5	Sequence 5, Appl
37	534	91.9	110	18	US-10-959-318-6	Sequence 6, Appl
38	534	91.9	110	18	US-10-959-318-25	Sequence 25, Appl
39	533	91.7	110	18	US-10-959-318-23	Sequence 23, Appl
40	533	91.7	110	18	US-10-959-318-24	Sequence 24, Appl
41	532	91.6	110	17	US-10-491-653-22	Sequence 22, Appl
42	528	90.9	102	18	US-10-609-783B-54	Sequence 54, Appl
43	526	90.5	102	18	US-10-609-783B-57	Sequence 57, Appl
44	526	90.5	102	18	US-10-609-783B-59	Sequence 59, Appl
45	524	90.2	110	18	US-10-959-318-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
US-10-959-318-11

Query Match 98.6%; Score 573; DB 18; Length 109;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60


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US-10-959-318-15
Query Match          96.2%; Score 559; DB 18; Length 109;
Best Local Similarity 96.3%; Pred. No. 4.4e-47;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 6
US-10-959-318-16
; Sequence 16, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and e (E268)
US-10-959-318-16

Query Match          96.2%; Score 559; DB 18; Length 109;
Best Local Similarity 96.3%; Pred. No. 4.4e-47;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSEDEPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 7
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-2

Query Match          95.4%; Score 554; DB 18; Length 109;
Best Local Similarity 93.6%; Pred. No. 1.4e-46;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 8
US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
US-10-959-318-13

Query Match          94.4%; Score 548.5; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 4.8e-46;
Matches 105; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Db 1 APPVAGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Qy 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 9
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
US-10-959-318-14

Query Match          94.4%; Score 548.5; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 4.8e-46;
Matches 105; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Db 1 APPVAGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Qy 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

```

```
/ SEQ ID NO 14
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)
US-10-959-318-14

Query Match          94.4%; Score 548.5; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 4.8e-46;
Matches 105; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Db 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60

QY 60 PREEQNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 109
Db 61 PREEQNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKALPAPIEKTSKAK 110

RESULT 10
US-10-959-318-7
/ Sequence 7, Application US/10959318
/ Publication No. US20050215768A1
/ GENERAL INFORMATION:
/ APPLICANT: Armour, Kathryn L
/ APPLICANT: Clark, Michael R
/ TITLE OF INVENTION: Polypeptides including modified constant regions
/ FILE REFERENCE: 39-302
/ CURRENT APPLICATION NUMBER: US/10/959,318
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: PCT/GB2004/004254
/ PRIOR FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: GB0324368.0
/ PRIOR FILING DATE: 2003-10-17
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 7
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
US-10-959-318-7

Query Match          94.3%; Score 548; DB 18; Length 110;
Best Local Similarity 97.2%; Pred. No. 5.3e-46;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKPREE 64

QY 64 QYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 109
Db 65 QYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 110

RESULT 11
US-10-959-318-8
/ Sequence 8, Application US/10959318
/ Publication No. US20050215768A1
/ GENERAL INFORMATION:
/ APPLICANT: Armour, Kathryn L
/ APPLICANT: Clark, Michael R
/ TITLE OF INVENTION: Polypeptides including modified constant regions
/ FILE REFERENCE: 39-302
/ CURRENT APPLICATION NUMBER: US/10/959,318
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: PCT/GB2004/004254
```

```
/ PRIOR FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: GB0324368.0
/ PRIOR FILING DATE: 2003-10-17
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 8
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268)
US-10-959-318-8

Query Match          94.3%; Score 548; DB 18; Length 110;
Best Local Similarity 97.2%; Pred. No. 5.3e-46;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKPREE 64

QY 64 QYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 109
Db 65 QYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 110

RESULT 12
US-10-627-556-270
/ Sequence 270, Application US/10627556
/ Publication No. US20050136049A1
/ GENERAL INFORMATION:
/ APPLICANT: LEDBETTER, JEFFREY A.
/ APPLICANT: HAYDEN-LEDBETTER, MARTHA
/ APPLICANT: THOMPSON, PETER A.
/ TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
/ FILE REFERENCE: 49076.000004.CIP2
/ CURRENT APPLICATION NUMBER: US/10/627,556
/ CURRENT FILING DATE: 2003-07-26
/ PRIOR APPLICATION NUMBER: 10/053,530
/ PRIOR FILING DATE: 2002-01-17
/ PRIOR APPLICATION NUMBER: 60/367,358
/ PRIOR FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/765,208
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/385,691
/ PRIOR FILING DATE: 2002-06-03
/ NUMBER OF SEQ ID NOS: 699
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 270
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-627-556-270

Query Match          94.1%; Score 547; DB 18; Length 109;
Best Local Similarity 96.2%; Pred. No. 6.6e-46;
Matches 102; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63

QY 64 QYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 109
Db 64 QYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKALPASIEKTSKAK 109

RESULT 13
US-10-959-318-17
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[illegible]

Search completed: November 17, 2005, 08:18:45
Job time : 82.3721 secs

		Query Match	94.0%	Score 546;	DB 18;	Length 109;
		Best Local Similarity	92.7%;	Pred. No.	8.3e-46;	
		Matches 101;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	APPVAGSVFLFPKPKDTL	MISRPTEVT	CVVVDVSHEDEPVEKFNNYVGVEVHNAKTGP	60	
Dd	1	APPVAGSVFLFPKPKDTL	MISRPTEVT	CVVVDVSSEDEPEVFNNYVGVEVHNAKTGP	60	
Qy	61	RREEYNSTYRVVSLTVL	VHQDWLNCKEYKCKYSNKGLPSSIEKTSKAK	109		
		:	:	:		
Dd	61	RREOFNSTFRVVSVLTV	VHQDWLNCKEYKCKYSNKGLPAPIEKTSKTK	109		
		:	:	:		

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 90.8333 Seconds
(without alignments)
464.112 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGSPVFLPPKPKDTL.....CKVSNKGLPSSIEKTSKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	100.0	326	8	ADF77155
2	580	100.0	447	8	ADQ17121 Humanised
3	580	100.0	462	8	ADF77154 Chimexic
4	577	99.5	436	7	ADM33853 Human HuE
5	577	99.5	436	8	ADR48984 HuEPO-L-F
6	577	99.5	448	7	ADM33376 Human GCS
7	572	98.6	109	2	AAR41709 Undefined
8	572	98.6	109	3	RAY54997 Mutated C
9	572	98.6	217	3	AAB07476 Amino aci
10	572	98.6	217	4	AAB76423 Human Igg
11	572	98.6	217	4	AAB67203 Human Igg
12	572	98.6	217	5	AAG78434 Native se
13	572	98.6	217	6	ABR42440 Human Igg
14	572	98.6	217	8	ADH75378 Human Igg
15	572	98.6	228	5	ABG31095 Human mat
16	572	98.6	228	8	ADR48993 Human Igg
17	572	98.6	310	8	ADR84436 Human ant
18	572	98.6	310	8	ADR68578 Human ant
19	572	98.6	326	4	AAE02643 Human imm
20	572	98.6	326	5	RAM47857 Human Ig-
21	572	98.6	326	5	ABG30462 Human ant
22	572	98.6	326	5	ABG77148 Anti-IGF-
23	572	98.6	326	6	AAE32916 Human imm
24	572	98.6	326	6	AAE32628 Human imm
25	572	98.6	326	6	AAO30894 Human imm

26	572	98.6	326	7	ADE97353	Adc97353 Human Igg
27	572	98.6	326	7	ADF75002	Adf75002 Human Igg
28	572	98.6	326	8	ADM41541	Adm41541 Anti-inte
29	572	98.6	326	8	ADQ95469	Adq95469 Human Igg
30	572	98.6	326	8	ADR28562	Adr28562 Human ant
31	572	98.6	381	2	AAY06895	Aay06895 Human IL-
32	572	98.6	432	2	AAR26782	Aar26782 CD4-gamma
33	572	98.6	432	2	AAR46678	Aar46678 CD4-gamma
34	572	98.6	432	3	AAY85079	Aay85079 Human CD4
35	572	98.6	432	4	AAB67322	Aab67322 CD4-gamma
36	572	98.6	432	4	AAB80883	Aab80883 Human CD4
37	572	98.6	432	6	ABG71122	Abg71122 CD4-gamma
38	572	98.6	442	4	AAB72230	Aab72230 Humanised
39	572	98.6	443	2	AAY31670	Aay31670 Human Igg
40	572	98.6	445	8	ADK52332	Adk52332 Human ant
41	572	98.6	445	8	ADK52384	Adk52384 Human ant
42	572	98.6	445	8	ADK52296	Adk52296 Human ant
43	572	98.6	445	8	ADK52312	Adk52312 Human ant
44	572	98.6	446	7	ADM18320	Adm18320 Human CD4
45	572	98.6	451	3	AAY93734	Aay93734 The heavy

ALIGNMENTS

RESULT 1
ADF77155
ID ADF77155 standard; protein; 326 AA.
XX
AC ADF77155;
XX
DT 26-FEB-2004 (first entry)
XX
DE Anti-VAP-1 monoclonal antibody H chain constant region.
XX
KW complementarity determining region; CDR; mouse;
KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
KW chimeric; inflammatory disorder; rheumatoid arthritis;
KW inflammatory bowel disease; autoimmune disease; psoriasis;
KW immunosclintigraphic imaging.
XX
OS Homo sapiens.
XX
PN WO2003093319-A1.
XX
PD 13-NOV-2003.
XX
PF 28-APR-2003; 2003WO-FI000330.
XX
PR 29-APR-2002; 2002FI-00000807.
XX
PA (BIOT-) BIOTIE THERAPIES CORP.
XX
PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;
XX
WPI; 2004-022642/02.
XX
PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
PT encoding nucleic acid molecules, useful for diagnosing and treating
PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
XX
PS Claim 18; SEQ ID NO 16; 56pp; English.
XX
CC This sequence represents the constant region of a human anti-Vascular
CC Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be
CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The
CC nucleic acid molecules, polypeptides or antibodies are useful in treating
CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,
CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
CC chimeric VAP-1 antibody is further used for in vitro and in vivo
CC diagnostic applications, including in vivo immunosclintigraphic imaging of
CC inflammation sites. The chimeric Mab's of the invention have improved
CC kinetic properties compared to the corresponding murine antibodies.

```

XX SQ Sequence 326 AA;
Query Match 100.0%; Score 580; DB 8; Length 326;
Best Local Similarity 100.0%; Pred. No. 9e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 60
Db 111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 170

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
Db 171 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 219

RESULT 2
ADQ17121
ID ADQ17121 standard; protein; 447 AA.
XX AC ADQ17121;
AC ADQ17121;
DT 07-OCT-2004 (first entry)
XX Humanised anti-NGF antibody E3 heavy chain full-length protein.
XX nerve growth factor; anti-NGF antibody; E13.5 trigeminal neurone;
KW analgesic; immunomodulator; post-surgical pain; rheumatoid arthritis;
KW osteoarthritis; inflammatory cachexia; gene therapy;
KW monoclonal antibody 911; humanised antibody E3; heavy chain; murine;
KW mouse; mutant; mutein.
XX Mus sp.
OS Homo sapiens.
OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 26..35
FT /note= "Extended CDR (complementarity determining region)
FT 1"
FT Misc-difference 34
FT /note= "Wild-type Ile of murine Mab 911 substituted by
FT Leu"
FT Region 50..65
FT /note= "Extended CDR (complementarity determining region)
FT 2"
FT Misc-difference 50
FT /note= "Wild-type Met of murine Mab 911 substituted by
FT Ile"
FT Misc-difference 63
FT /note= "Wild-type Leu of murine Mab 911 substituted by
FT Val"
FT Region 98..110
FT /note= "Extended CDR (complementarity determining region)
FT 3"
FT Misc-difference 101
FT /note= "Wild-type Tyr of murine Mab 911 substituted by
FT Trp"
FT Misc-difference 103
FT /note= "Wild-type Gly of murine Mab 911 substituted by
FT Ala"
XX WO2004058184-A2.
XX 15-JUL-2004.
XX 24-DEC-2003; 2003WO-US041252.
XX 24-DEC-2002; 2002US-0436905P.
PR 28-JAN-2003; 2003US-0443522P.
PR 08-OCT-2003; 2003US-0510006P.
XX (RINA-) RINAT NEUROSCIENCE CORP.
PA

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XX PI Shelton DL, Pons J, Rosenthal A;
XX WPI; 2004-525786/50.
DR N-PSDB; ADQ17170.
XX New anti-nerve growth factor antibodies for preventing or treating pain,
PT including post-surgical pain, rheumatoid arthritis pain or osteoarthritis
PT pain, or for treating inflammatory cachexia associated with rheumatoid
PT arthritis.
XX Claim 25; SEQ ID NO 16; 186pp; English.
XX The invention relates to a novel anti-nerve growth factor (NGF) antibody
XX which binds NGF with a KD of less than about 2 nM and inhibits human NGF-
CC dependent survival of mouse E13.5 trigeminal neurones with an IC50 of
CC about 100 or 10 pM or less, where the IC50 is measured in the presence of
CC about 15 or 1.5 pM of human NGF. The antibody of the invention
CC demonstrates analgesic and immunomodulator activities and may be useful
CC for preventing and/or treating pain, including post-surgical pain and
CC pain associated with rheumatoid arthritis or osteoarthritis. The antibody
CC may be further utilised for treating inflammatory cachexia associated
CC with rheumatoid arthritis, as well as during gene therapy procedures. The
CC current sequence is that of the humanised anti-NGF antibody E3 heavy
CC chain full-length protein of the invention which was synthesised via
CC grafting CDRs (complementarity determining regions) from murine anti-NGF
CC Mab (monoclonal antibody) 911 onto human framework sequences and
CC subsequently mutating the CDRs to improve binding.
XX SQ Sequence 447 AA;
Query Match 100.0%; Score 580; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 60
Db 232 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 291

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
Db 292 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 340

RESULT 3
ADF77154
ID ADF77154 standard; peptide; 462 AA.
XX AC ADF77154;
XX 26-FEB-2004 (first entry)
XX Chimeric Anti-VAP-1 monoclonal antibody H chain.
DE Complementarity determining region; CDR; mouse;
XX Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
KW chimeric; inflammatory disorder; rheumatoid arthritis;
KW inflammatory bowel disease; autoimmune disease; psoriasis;
KW immunoscintigraphic imaging.
XX Chimeric.
OS Mus sp.
OS Homo sapiens.
XX WO2003093319-A1.
XX 13-NOV-2003.
XX 28-APR-2003; 2003WO-FI000330.
XX 29-APR-2002; 2002FI-00000807.
XX (BIOT-) BIOTIE THERAPIES CORP.
PA

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XX PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;
XX WPI; 2004-022642/02.
DR N-PSDB; ADF77144.
XX
XX New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
XX encoding nucleic acid molecules, useful for diagnosing and treating
XX chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
XX
XX Claim 9; SEQ ID NO 15; 56pp; English.
XX
XX This sequence represents a chimeric human-mouse anti-Vascular Adhesion
XX protein-1 (VAP-1) antibody heavy chain. This sequence may be used in the
XX production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic
XX acid molecules, polypeptides or antibodies are useful in treating VAP-1
XX mediated inflammatory disorders, such as rheumatoid arthritis,
XX inflammatory bowel disease, autoimmune diseases or psoriasis. The
XX chimeric VAP-1 antibody is further used for in vitro and in vivo
XX diagnostic applications, including in vivo immunoscinographic imaging of
XX inflammation sites. The chimeric MAB's of the invention have improved
XX kinetic properties compared to the corresponding murine antibodies.
XX
XX Sequence 462 AA;
XX
XX Query Match 100.0%; Score 580; DB 8; Length 462;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-50;
XX Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 60
XX 247 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 306
XX
XX 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
XX 307 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 355
XX
XX
XX RESULT 4
XX ADM33853
XX ID ADM33853 standard; protein; 436 AA.
XX
XX AC ADM33853;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human HuEPO-L-vFc gamma2 fusion protein.
XX
XX Erythropoietin; EPO; immunoglobulin; IgG;
XX fragment crystallisation region; Fc; chronic anaemia; renal disease;
XX cancer chemotherapy; rheumatoid arthritis; AIDS;
XX myelodysplastic syndrome; (HuEPO)-L-vFc gamma2; human.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..27
XX /note= "Signal peptide"
XX Protein 28..192
XX /note= "EPO"
XX Peptide 193..208
XX /note= "Linker"
XX Protein 209..436
XX /note= "IgG2 Fc"
XX Misc-difference 390
XX /note= "Wild-type Pro substituted by Ser"
XX
XX US2003082749-A1.
XX
XX 01-MAY-2003.
XX
XX 17-AUG-2001; 2001US-00932812.
XX
XX
XX 17-AUG-2001; 2001US-00932812.
XX
XX (SUNL/) SUN L K.
XX (SUNB/) SUN B N C.
XX (SUNC/) SUN C R Y.
XX
XX Sun LK, Sun BNC, Sun CRY;
XX
XX WPI; 2003-616080/58.
XX
XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for
XX treating patients with chronic anemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
XX infection.
XX
XX Claim 3; Fig 2A; 14pp; English.
XX
XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
XX fusion protein comprising HuEPO, a peptide linker, and a human
XX immunoglobulin G Fc (fragment crystallisation region) variant. Also
XX included is a carbohydrate-derived cell line producing the human
XX erythropoietin-L-vFc fusion protein cited above in its growth medium in
XX excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
XX -L-vFc fusion protein exhibits an enhanced in vitro biological activity
XX of at least 2-fold relative to that of recombinant HuEPO on a molar
XX basis. The flexible peptide linker containing about 20 or fewer amino
XX acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
XX contains amino acid mutations to attenuate effector functions. The human
XX IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
XX human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The
XX Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
XX recombinant human erythropoietin-L-vFc fusion proteins are useful for
XX treating patients with chronic anaemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
XX infection, or myelodysplastic syndrome. The increased activity and
XX prolonged presence of the human erythropoietin-L-vFc fusion protein in
XX the serum, as compared to prior art, leads to lower dosages and less
XX frequent injections. Less fluctuations of the drug in serum
XX concentrations means improved safety and tolerability, and less frequent
XX injections result in better patient compliance and quality of life. The
XX present sequence represents the fusion protein HuEPO-L-vFc gamma2.
XX
XX Sequence 436 AA;
XX
XX Query Match 99.5%; Score 577; DB 7; Length 436;
XX Best Local Similarity 99.1%; Pred. No. 2.6e-50;
XX Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 60
XX 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 280
XX
XX 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
XX 281 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 329
XX
XX
XX RESULT 5
XX ADR48984
XX ID ADR48984 standard; protein; 436 AA.
XX
XX AC ADR48984;
XX
XX 02-DEC-2004 (first entry)
XX
XX HuEPO-L-Fc fusion protein.
XX
XX antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
XX anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
XX AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
XX
XX Homo sapiens.
XX

```

OS Synthetic.
 PN US2004175824-A1.
 XX 09-SEP-2004.
 PD
 XX 21-JAN-2004; 2004US-00761593.
 XX 17-AUG-2001; 2001US-00932812.
 XX (SUNL/) SUN L K.
 PA (SUNB/) SUN B N C.
 PA (SUNC/) SUN C R Y.
 XX
 XX Sun LK, Sun BNC, Sun CRY;
 XX WPI: 2004-634851/61.
 DR N-PSDB; ADR48983.
 XX
 XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.
 PT
 PT
 PT
 XX Claim 3; SEQ ID NO 18; 31pp; English.
 PS
 XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, is new.
 CC INDEPENDENT CLAIMS are also included for the following: a Chinese hamster ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in its growth medium in excess of 10 μ microg/g per million cells in a 24 hour period; and a method for making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred Protein: The peptide linker containing 20 or fewer amino acids is present between HuEPO and the human IgG Fc variant, and comprises two or more amino acids selected from glycine, serine, alanine, and threonine. The human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18). It also comprises a hinge, CH2, and CH3 domains of human IgG4 with Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO. 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1 with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 435 amino acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line producing the HuEPO-L-vFc fusion protein in its growth medium in excess of 30 μ microg/g per million cells in a 24 hour period. The human IgG Fc variant comprises a hinge, CH2, CH3 domains of human IgG selected from IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, the IgG Fc contains amino acid mutations to attenuate effector functions, a flexible peptide linker containing 20 or fewer amino acids is present between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred Method: Making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant comprises: Generating a CHO-derived cell line; growing the cell line where the recombinant protein is expressed in its growth medium in excess of 10 μ microg/g per million cells in a 24 hour period; and purifying the expressed protein from (b), where the recombinant fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological data given. None given. Administration can be through subcutaneous or intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion protein is useful for treating patients with chronic anemia due to renal diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for HIV infection, or myelodysplastic syndrome. It is also useful in the treatment of renal failure. A fusion protein was assembled from several DNA segments. To obtain the gene encoding the leader peptide and mature protein of human erythropoietin (EPO), cDNA library of human fetal liver or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon

CC and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pPEO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.
 CC
 XX
 SQ Sequence 436 AA;
 Query Match 99.5%; Score 577; DB 8; Length 436;
 Best Local Similarity 99.1%; Pred. No. 2.6e-50;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
 DB 221 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 280
 QY 61 REEQFNSTFRVSVLTIVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
 DB 281 REEQFNSTFRVSVLTIVVHQDWLNGKEYKCKVSNKGLPASIETIKTK 329
 RESULT 6
 ADM33376
 ID ADM33376 standard; protein; 448 AA.
 XX AC ADM33376;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human GCSF-L-fragment of crystallisation gamma 2 fusion protein.
 XX KW cyostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;
 KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;
 KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;
 KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;
 KW bone marrow transplantation; chronic neutropenia; fusion protein;
 KW fragment of crystallisation gamma 2; Fc gamma 2.
 XX OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Peptide 1..30 /label= GCSF leader peptide
 FT Protein 31..448 /note= "Mature human GCSF-L-fragment of crystallisation gamma 2 fusion"
 FT Misc-difference 331 /note= "Wild type Pro substituted by Ser"
 FT US2003082679-A1.
 PN 01-MAY-2003.
 PD 01-OCT-2001; 2001US-00968362.
 XX 01-OCT-2001; 2001US-00968362.
 XX (SUNL/) SUN L K.
 PA (SUNB/) SUN B N C.
 PA (SUNC/) SUN C R Y.
 XX Sun LK, Sun BNC, Sun CRY;
 XX WPI: 2003-585400/55.
 DR N-PSDB; ADM33375.
 XX
 XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-vFc fusion protein for treating immune or hematopoietic system disorders comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G Fc variant.
 PT
 XX Disclosure; Fig 2A; 15pp; English.
 PS
 XX

capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FcγmacR1b causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of graft-vs-host disease, organ transplant rejection, bone-marrow transplant rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia and arthritis), autoimmunity (e.g. foetal/neonatal alloimmune thrombocytopenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HBN (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FcγmacR1 and desirable IgG properties have been retained. The polypeptides do not contain non-human amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FcRn (neonatal Fc receptor)

XX Sequence 109 AA;

Query Match 98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 99.1%; Pred. No. 1.6e-50;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

QY 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

Db 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 9

AAB07476

ID AAB07476 standard; protein; 217 AA.

XX AAB07476;

AC AAB07476;

DT 20-OCT-2000 (first entry)

DE Amino acid sequence of native IgG Fc region humIgG2.

XX IgG antibody; light chain; Fc region; effector function; cancer; allergy;

KW asthma; LFA-1-mediated disorder; tumour; cancer.

XX Homo sapiens.

OS WO200042072-A2.

PN 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US000973.

PF 15-JAN-1999; 99US-0116023P.

XX (GETH) GENENTECH INC.

PA Presta LG;

PI WPI; 2000-476035/41.

XX New Fc region-containing polypeptides that have altered effector function

PT due to one or more amino acid modifications in the Fc region, useful in

PT the treatment of cancer and allergic conditions such as asthma.

XX Disclosure; Fig 22A; 132pp; English.

PS

XX AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1 disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer

XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 3; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

QY 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 110

RESULT 10

AAB76423

ID AAB76423 standard; protein; 217 AA.

XX AAB76423;

AC AAB76423;

XX 10-APR-2001 (first entry)

DE Human IgG2 Fc region amino acid sequence.

XX Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;

KW metabolic disorder; nutritional deficiency; Alzheimer's disease;

KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;

KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.

XX Homo sapiens.

OS WO200101748-A2.

PN 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US018283.

PF 02-JUL-1999; 99US-0142232P.

XX (GETH) GENENTECH INC.

PA Dennis MS;

PI WPI; 2001-123048/13.

XX Non-naturally occurring peptide ligands which compete for binding human

PT erbB2 gene products, useful for treating e.g. Alzheimer's disease,

PT multiple sclerosis and diabetic neuropathy.

XX Disclosure; Fig 2A; 116pp; English.

PS This invention relates to non-naturally occurring peptide ligands which

CC bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides

CC represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples

CC of the ErbB2 binding ligands of the invention. Sequences AAB76421 -

AAH76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculoskeletal and epithelial, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.

XX
SQ Sequence 217 AA;

Query Match 98.6%; Score 572; DB 4; Length 217;

Query Match 50.0%, Score 37, DB #, DB #,
Best Local Similarity 98.2%; Pred. No. 3.6e-50;

Best Local Similarity 98.2%, Freq. NO: 3.0E-30;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	APVAGSGSVFLPPKPKD	TLMTLSRTP	EVTCVVVDVSHEDPE	VFQFNWYDGVGVHNAK	TKP	60
Db	2	APVAGSGSVFLPPKPKD	TLMTLSRTP	EVTCVVVDVSHEDPE	VFQFNWYDGVGVHNAK	TKP	61
Qy	61	REEQFNSTFRVSVLTV	FWHQDMLNGKEYK	CKVSNKGLPSS	EKTI	SKTK	109
Db	62	REEQFNSTFRVSVLTV	FWHQDMLNGKEYK	CKVSNKGLPAP	EKTI	SKTK	110

RESULT 11

RESOLUTION 11
AAB67203
ID AAB67203 standard; protein; 217 AA.

AC AAB67203:

DT 10-APR-2000

XX
DE Human IgG2.

KW Fusion protein; immunoglobulin; multidimerization domain; ligand.

OS Homo sapiens.

AA
PN
WO200102440-A1.

11-JAN-2001.

30-JUN-2000: 2000WO-US018185.

AA 02-JUL-1999; 99US-0142088P.

AA (GETH) GENENTECH INC.

PI Dennis MS, Lazarus RA;

WPI; 2001-123106/13.

Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain.

PS Disclosure: Fig 2: 69pp; English.

xx The present invention relates to a fusion protein, comprising a peptide
CC ligand and an immunoglobulin (Ig) constant region multimerization domain
CC (f1b). The hybrid molecules comprising the peptide ligands and their
CC functional derivatives can be used in the same applications as, a peptide
CC ligand can be used. For example the peptide ligand can bind ErbB3. A
CC peptide ligand may bind to and inhibit the activity associated with a
CC particular target molecule

Sequence 217 AA;

Query Match 98.6%; Score 572; DB 4; Length 217;

Best Local Similarity 98.2%; Pred. No. 3.6e-50;

[illegible]

RESULT 12

AAG78434

ID AAG78434 standard; protein; 217 AA.

AC AAG78434;

DT 12-APR-2002 (first entry)

XX	DE	Native sequence	human IgG	Fc region sequence	humIgG2.
1	1	1	1	1	1
2	2	2	2	2	2
3	3	3	3	3	3
4	4	4	4	4	4
5	5	5	5	5	5
6	6	6	6	6	6
7	7	7	7	7	7
8	8	8	8	8	8
9	9	9	9	9	9
10	10	10	10	10	10
11	11	11	11	11	11
12	12	12	12	12	12
13	13	13	13	13	13
14	14	14	14	14	14
15	15	15	15	15	15
16	16	16	16	16	16
17	17	17	17	17	17
18	18	18	18	18	18
19	19	19	19	19	19
20	20	20	20	20	20
21	21	21	21	21	21
22	22	22	22	22	22
23	23	23	23	23	23
24	24	24	24	24	24
25	25	25	25	25	25
26	26	26	26	26	26
27	27	27	27	27	27
28	28	28	28	28	28
29	29	29	29	29	29
30	30	30	30	30	30
31	31	31	31	31	31
32	32	32	32	32	32
33	33	33	33	33	33
34	34	34	34	34	34
35	35	35	35	35	35
36	36	36	36	36	36
37	37	37	37	37	37
38	38	38	38	38	38
39	39	39	39	39	39
40	40	40	40	40	40
41	41	41	41	41	41
42	42	42	42	42	42
43	43	43	43	43	43
44	44	44	44	44	44
45	45	45	45	45	45
46	46	46	46	46	46
47	47	47	47	47	47
48	48	48	48	48	48
49	49	49	49	49	49
50	50	50	50	50	50
51	51	51	51	51	51
52	52	52	52	52	52
53	53	53	53	53	53
54	54	54	54	54	54
55	55	55	55	55	55
56	56	56	56	56	56
57	57	57	57	57	57
58	58	58	58	58	58
59	59	59	59	59	59
60	60	60	60	60	60
61	61	61	61	61	61
62	62	62	62	62	62
63	63	63	63	63	63
64	64	64	64	64	64
65	65	65	65	65	65
66	66	66	66	66	66
67	67	67	67	67	67
68	68	68	68	68	68
69	69	69	69	69	69
70	70	70	70	70	70
71	71	71	71	71	71
72	72	72	72	72	72
73	73	73	73	73	73
74	74	74	74	74	74
75					

Antibody; antigen; immunoglobulin; ADCC; CDC; anti-globin response;
antibody dependant cell mediated cytotoxicity;
complement dependant cytotoxicity; epidermal growth factor receptor;
tumour necrosis factor; lymphocyte; tetraivalent antibody; cytostatic;
antiinflammatory; antipsoriatic; dermatological; antiulcer;
antiasthmatic; antiarteriosclerotic; antirheumatic; antibacterial;
antiarrhythmic; neuroprotective; immunosuppressive; antianemic;
antiallergic; antidiabetic; gene therapy; human.

OS Homo sapiens.

AA
PN
WO200177342-A1.XX
PD
18-OCT-2001.

XX
PF 20-MAR-2001: 2001WO-US008928.

XX
PR 11-APR-2000; 2000US-0195819P.

AA (GETH) GENENTECH INC.
PA

XX
PI
Miller KL, Presta LG:

AA
DR WPI; 2002-049149/06.

Novel engineered antibody useful in therapeutic applications, contains a dimerization domain and three or more antigen binding sites.

XX PS Disclosure: Fig 3: 186pp: English.

This invention relates to an isolated antibody comprising a dimerisation domain and three or more antigen binding sites amino-terminal to the domain. It is cytostatic, antiinflammatory, antibacterial, immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used in gene therapy. Along with a cytotoxic agent, is useful for treating a disorder e.g. cancer in a mammal, for inducing apoptosis of a cancer cell, and for killing a B cell or a cell which overexpresses or expresses an ErbB receptor and for treating benign and malignant tumours, inflammatory, angiogenic and immunological disorders, autoimmune diseases, central nervous system inflammatory disorders. The antibody is also useful for immunodiagnosis of various diseases including cancer, for human therapy in redirected cytotoxicity, and also useful as fibrinolytic agents or vaccine adjuvants, useful as affinity purification agent, in diagnostic assays for detecting the expression of antigen of interest in specific cells, tissue or serum, and useful for blocking an immune response to a foreign antigen. The antigen is internalised faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibody comprises three or four heavy chain variable domains which are able to combine with three or four light chain variable domain polypeptides to form three or four antigen binding sites directed against the same antigen. This sequence represents the native sequence human IgG FC region, humiqg2

```
XX SQ Sequence 217 AA;
Query Match 98.6%; Score 572; DB 5; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 109
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 110

RESULT 13
ABR42440
ID ABR42440 standard; protein; 217 AA.
XX AC ABR42440;
XX DT 11-AUG-2003 (first entry)
XX DE Human IgG2 Fc region.
XX KW Human; antibody; IgG2; cytostatic; immunosuppressive; antiinflammatory; antimicrobial.
XX OS Homo sapiens.
XX PN W02003035835-A2.
XX PD 01-MAY-2003.
XX PF 22-OCT-2002; 2002WO-US033739.
XX PR 25-OCT-2001; 2001US-0337642P.
XX PR 09-JAN-2002; 2002US-0347694P.
XX PA (GETH ) GENENTECH INC.
XX PI Presta IG;
XX WPI; 2003-421411/39.
XX New composition comprising a glycoprotein having a Fc region useful for treating cancer, autoimmune disease, inflammatory disorder or infection in a mammal.
XX Disclosure; Fig 23; 139pp; English.
XX The present sequence is the protein sequence of the Fc region of human IgG2. A claimed composition comprises a glycoprotein having a Fc region. About 80-100% of the glycoprotein comprises a mature core carbohydrate structure which lacks fucose attached to the Fc region. The glycoprotein preferably comprises an antibody, and the Fc region is preferably a human IgG Fc region, especially a human IgG1, IgG2, IgG3 or IgG4 Fc region. The glycoprotein binds Fc gammaRIII with better affinity, or mediates antibody dependent cell-mediated cytotoxicity more effectively, than the human and binds a B-cell surface marker, an ErbB receptor, a tumour-associated antigen or an angiogenic factor, CD20, HER2, vascular endothelial growth factor, CD40 or prostate stem cell antigen. The composition is useful for treating cancer, autoimmune disease, an inflammatory disorder or infection in a mammal
XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 6; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 110

RESULT 15
ABG31095
ID ABG31095 standard; protein; 228 AA.
XX
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Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 110

RESULT 14
ADH75378
ID ADH75378 standard; protein; 217 AA.
XX AC ADH75378;
XX DT 22-APR-2004 (first entry)
XX DE Human IgG2.
XX KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
XX OS Homo sapiens.
XX PN US2004002587-A1.
XX PD 01-JAN-2004.
XX PF 20-FEB-2003; 2003US-00370749.
XX PR 20-FEB-2002; 2002US-0358161P.
XX PA (WATK/) WATKINS J D.
XX PA (ALLA/) ALLAN B.
XX PI Watkins JD, Allan B;
XX WPI; 2004-070755/07.
XX New composition comprising a variant of a parent polypeptide having at least a portion of a Fc region, useful in treating e.g., autoimmune diseases.
XX Disclosure; SEQ ID NO 16; 62pp; English.
XX The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the Fc region. The composition is useful in treating diseases e.g., acid autoimmune diseases. The present sequence represents the amino acid sequence of a human immunoglobulin G, IgG.
XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 8; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 110

RESULT 15
ABG31095
ID ABG31095 standard; protein; 228 AA.
XX
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:49:37 ; Search time 17.9178 Seconds
(without alignments)
585.319 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGPSVFLPPPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	326	1 G2HU	Ig gamma-2 chain C
2	536	92.4	327	1 G4HU	Ig gamma-4 chain C
3	529	91.2	377	2 A23511	Ig gamma-3 chain C
4	529	91.2	377	2 A60764	Ig gamma-3 chain C
5	526	90.7	234	2 PT0207	Ig gamma chain C r
6	524	90.3	255	4 S31866	Ig gamma-1 chain C
7	524	90.3	330	1 GHU	Ig gamma-1 chain C
8	524	90.3	374	2 S69339	Ig heavy chain v r
9	516	89.0	289	1 G3HUM1	Ig gamma-3 heavy c
10	457	78.8	328	2 I47160	Ig gamma 2b chain
11	457	78.8	328	2 I47159	Ig gamma 2a chain
12	452	77.9	277	2 I47162	Ig gamma 4 chain c
13	441	76.0	328	2 I47161	Ig gamma 3 chain c
14	441	76.0	328	2 I47158	Ig gamma 1 chain c
15	429	74.0	470	2 S22080	Ig heavy chain pre
16	425	73.3	308	2 C30554	Ig heavy chain C r
17	425	73.3	329	1 G2GP	Ig gamma-2 chain C
18	425	73.3	472	2 S31459	Ig gamma-1 chain -
19	423	72.9	333	2 PS0018	Ig gamma-2b chain
20	418	72.1	323	1 GHRB	Ig gamma chain C r
21	414	71.4	327	2 S06611	Ig gamma-2 chain C
22	410.5	70.8	329	1 G3MSC	Ig gamma-3 chain C
23	410.5	70.8	398	1 G3MSM	Ig gamma-3 chain C
24	410	70.7	324	1 G1MS	Ig gamma-1 chain C
25	410	70.7	393	1 G1MSM	Ig gamma-1 chain C
26	410	70.7	444	2 PC4336	monoclonal antibod
27	400	69.0	329	2 S00847	Ig gamma-2c chain
28	384	66.2	326	2 PS0017	Ig gamma-1 chain C
29	383	66.0	335	1 G2MSAB	Ig gamma-2a chain

RESULT 1
G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93132; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co

A:Reference number: A93906; MUID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1;

A>Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Contents: myeloma protein Til

A:Accession: A92809

A:Molecule type: protein

A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>

A>Note: Trp-156 is at or near the complement-binding site

R:Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:80001357; PMID:113060

A:Contents: myeloma protein Zie

A:Accession: A90752

A:Molecule type: protein

A:Residues: 1-24,'E',26-57,'BV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198

A>Note: This sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A:Reference number: A93132; MUID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidate

ned

R:Milstien, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:127-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 98.6%; Score 572; DB 1; Length 326;
Best Local Similarity 98.2%; Pred. No. 6.1e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 111 APPVAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 170

Qy 61 REEQNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
Db 171 REEQNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTIKTK 219

RESULT 2
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant I

R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:127-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 92.4%; Score 536; DB 1; Length 327;
Best Local Similarity 94.3%; Pred. No. 2.6e-46;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 115 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 174

Qy 64 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
Db 175 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 220

RESULT 3
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: C
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.2%; Score 529; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 1.5e-45;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 165 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 224

Qy 64 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
Db 225 QYNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTIKTK 270

RESULT 4
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.2%; Score 529; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 1.5e-45;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 457; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 2.3e-38;
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
DB 116 GPSVFIFPPPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 175

QY 66 NSTFRVSVLTIVHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 109
DB 176 NSTYRVSVLPIQHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 219

RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 457; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 2.3e-38;
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
DB 116 GPSVFIFPPPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 175

QY 66 NSTFRVSVLTIVHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 109
DB 176 NSTYRVSVLPIQHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 219

RESULT 12
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 452; DB 2; Length 277;
Best Local Similarity 77.9%; Pred. No. 5.9e-38;
Matches 81; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
DB 65 GPSVFIFPPPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 124

QY 66 NSTFRVSVLTIVHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 109
DB 125 NSTYRVSVLPIQHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 168

RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47161
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C:Genetics:
A:Gene: IgG3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 441; DB 2; Length 328;
Best Local Similarity 77.9%; Pred. No. 9.2e-37;
Matches 81; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
DB 114 VAGPSVFIFPPPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 173

QY 64 QFNSTFRVSVLTIVHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 107
DB 174 QFNSTYRVSVLPIQHODWLNKGEYKCKVSNKGLPSSIEKTIISKTK 217

RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47158
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C:Genetics:
A:Gene: IgG1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 79.8936 Seconds
(without alignments)
698.725 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGPSVFLPPPKDPTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_prot:*

2: uniprot_treml:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	326	1 GC2 HUMAN	P01859 homo sapien
2	572	98.6	417	2 Q6N093	Q6N093 homo sapien
3	572	98.6	465	2 Q6P6C4	Q6P6C4 homo sapien
4	569	98.1	464	2 Q6MZU6	Q6MZU6 homo sapien
5	563	97.1	493	2 Q68CN4	Q68CN4 homo sapien
6	539	92.9	476	2 Q6WZV7	Q6WZV7 homo sapien
7	536	92.4	327	1 GC4 HUMAN	P01861 homo sapien
8	536	92.4	473	2 Q8TC63	Q8TC63 homo sapien
9	532	91.7	509	2 Q8NF17	Q8NF17 homo sapien
10	532	91.7	521	2 Q8N4Y9	Q8N4Y9 homo sapien
11	529	91.2	354	2 Q86TT2	Q86TT2 homo sapien
12	529	91.2	518	2 Q6N030	Q6N030 homo sapien
13	524	90.3	330	1 GC1 HUMAN	P01857 homo sapien
14	524	90.3	348	2 Q6PFX1	Q6PFX1 homo sapien
15	524	90.3	465	2 Q6GKX6	Q6GKX6 homo sapien
16	524	90.3	466	2 Q6IN78	Q6IN78 homo sapien
17	524	90.3	469	2 Q727P5	Q727P5 homo sapien
18	524	90.3	470	2 Q6PJA4	Q6PJA4 homo sapien
19	524	90.3	470	2 Q725W1	Q725W1 homo sapien
20	524	90.3	472	2 Q6N089	Q6N089 homo sapien
21	524	90.3	473	2 Q6MZV7	Q6MZV7 homo sapien
22	524	90.3	473	2 Q6P055	Q6P055 homo sapien
23	524	90.3	475	2 Q6GMW7	Q6GMW7 homo sapien
24	524	90.3	475	2 Q6WZQ6	Q6WZQ6 homo sapien
25	524	90.3	475	2 Q6N095	Q6N095 homo sapien
26	524	90.3	476	2 Q6GMX1	Q6GMX1 homo sapien
27	524	90.3	478	2 Q6P181	Q6P181 homo sapien
28	524	90.3	480	2 Q6N094	Q6N094 homo sapien
29	524	90.3	480	2 Q6P1F1	Q6P1F1 homo sapien
30	524	90.3	481	2 Q6N097	Q6N097 homo sapien
31	524	90.3	482	2 Q72351	Q72351 homo sapien

32	524	90.3	544	2	Q6PJ95	Q6PJ95 homo sapien
33	524	90.3	679	2	Q96FQ8	Q96FQ8 homo sapien
34	521	89.8	466	2	Q6N096	Q6N096 homo sapien
35	519	89.5	487	2	Q65ZL2	Q65ZL2 mus sp. fv/
36	516	89.0	290	1	GC3 HUMAN	P01860 homo sapien
37	443	76.4	337	2	Q95M34	Q95M34 equus cabal
38	425	73.3	329	1	GC2 CAVPO	P01862 cavia porce
39	423	72.9	333	1	GC5 RAT	P20761 rattus norv
40	418	72.1	323	1	GC RAMIT	P01870 oryctolagus
41	410.5	70.8	303	2	Q6KAM2	Q6KAM2 mus musculu
42	410.5	70.8	329	1	GC3 MOUSE	P22436 mus musculu
43	410.5	70.8	398	1	GC3M MOUSE	P03987 mus musculu
44	410.5	70.8	470	2	Q7TMK1	Q7TMK1 mus musculu
45	410	70.7	324	1	GC1_MOUSE	P01868 mus musculu

ALIGNMENTS

RESULT 1
GC2_HUMAN STANDARD; PRT; 326 AA.
ID GC2_HUMAN
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE I9 gamma-2 chain C region.
GN Name=IGHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";
RT Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
RN [3]
RL Cell 29:671-679(1982).
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=1131060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;


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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDB9348ADC37E6D CRC64;

Query Match 98.6%; Score 572; DB 2; Length 465;
Best Local Similarity 98.2%; Pred. No. 8.2e-49;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNATKP 60
Db 250 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNATKP 309
QY 61 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109
Db 310 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPAPIEKTIKTK 358

RESULT 4
Q6MZU6 PRELIMINARY; PRT; 464 AA.
ID Q6MZU6
AC Q6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

Query Match 98.1%; Score 569; DB 2; Length 464;
Best Local Similarity 97.2%; Pred. No. 1.6e-48;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNATKP 60
Db 249 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNATKP 308
QY 61 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109
Db 309 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPAPIEKTIKTK 357

RESULT 5
Q68CN4 PRELIMINARY; PRT; 493 AA.
ID Q68CN4
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RP TISSUE=Human rectum tumor;
RC The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C6688A0ABC CRC64;

Query Match 97.1%; Score 563; DB 2; Length 493;
Best Local Similarity 97.2%; Pred. No. 1.6e-48;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNATKP 60
Db 249 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNATKP 308
QY 61 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109
Db 309 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPAPIEKTIKTK 357

RESULT 5
Q68CN4 PRELIMINARY; PRT; 493 AA.
ID Q68CN4
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RP TISSUE=Rectum tumor;
RC The German cDNA Consortium;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 493 AA; 54117 MW; A1B4F5ED3FABAB40 CRC64;

Query Match 97.1%; Score 563; DB 2; Length 493;
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Best Local Similarity 96.3%; Pred. No. 7e-48; Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
 Db 278 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 337
 QY 61 REEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIISKTK 109
 Db 338 REEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIEKTIISKTK 386

RESULT 6

Q6MZKX7
 ID Q6MZKX7 PRELIMINARY; PRT; 476 AA.
 AC Q6MZKX7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686M24218.
 GN Name=DKFZp686M24218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human CDNA Consortium;
 RA Bloesker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RL Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640824; CAE45900.1; -;
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;

Query Match 92.9%; Score 539; DB 2; Length 476;
 Best Local Similarity 95.3%; Pred. No. 1.7e-45;
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTPREE 63
 Db 264 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTPREE 323

QY 64 QFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIISKTK 109
 Db 324 QFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIISKAK 369

RESULT 7

GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN Name=IGHG4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RN SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A90933; G4HU.
 DR PDB; IADQ; X-ray; A=118-323.
 DR Genew; HGNC:5528; IGHG4.
 DR MIM; 147130; -;
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
 KW Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 Hinge.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 Interchain (with a light chain).
 FT DISULFID 27 83 Interchain (with a heavy chain).
 FT DISULFID 106 106 Interchain (with a heavy chain).
 FT DISULFID 109 109 Interchain (with a heavy chain).
 FT DISULFID 141 201 Interchain (with a heavy chain).
 FT DISULFID 247 305 Interchain (with a heavy chain).
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811BF208E7A CRC64;
 Query Match 92.4%; Score 536; DB 1; Length 327;
 Best Local Similarity 94.3%; Pred. No. 2.2e-45;
 Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 4 VAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTPREE 63
 Db 115 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTPREE 174
 QY 64 QFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIISKTK 109
 Db 175 QFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIISKAK 220
 RESULT 8
 Q8TC63
 ID Q8TC63 PRELIMINARY; PRT; 473 AA.
 AC Q8TC63;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -;
DR HSSP; P01861; IADG.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 92.4%; Score 536; DB 2; Length 473;
Best Local Similarity 94.3%; Pred. No. 3.4e-45;
Matches 100; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 VAGPSVFLPPPKDPTLMISRTPVTCVVVDVSHEDPEVQFNWYDGVVHNAKTPREE 63
Db 261 LGGPSVFLPPPKDPTLMISRTPVTCVVVDVSHEDPEVQFNWYDGVVHNAKTPREE 320
QY 64 QFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 321 QFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 366
RESULT 9
Q8NF17
ID Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ00385 protein (Fragment).
GN Name=FLJ00385;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090464; BAC03445.1; -;
DR PIR; A45874; A45874.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 509 AA; 56110 MW; 089498D8076E863C CRC64;
Query Match 91.7%; Score 532; DB 2; Length 509;
Best Local Similarity 93.4%; Pred. No. 9.2e-45;
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 VAGPSVFLPPPKDPTLMISRTPVTCVVVDVSHEDPEVQFNWYDGVVHNAKTPREE 63
Db 228 LGGPSVFLPPPKDPTLMISRTPVTCVVVDVSHEDPEVQFNWYDGVVHNAKTPREE 287
QY 64 QFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 288 QFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETIKTK 333
RESULT 10
Q8N4Y9
ID Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC033178; AAH33178.1; -.
DR PIR; A60764; A60764.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match          91.7%; Score 532; DB 2; Length 521;
Best Local Similarity 93.4%; Pred. No. 9.5e-45;
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 309 LGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 368
QY 64 QNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
DQ 369 QNSTFRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTIKTK 414

RESULT 11
Q86TT2 PRELIMINARY; PRT; 354 AA.
AC Q86TT2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0D1019F20 of Placenta of Homo sapiens
DE (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Placenta;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=Placenta;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248278; CAD62606.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;

Query Match          91.2%; Score 529; DB 2; Length 354;
Best Local Similarity 92.5%; Pred. No. 1.2e-44;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 142 LGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 201
QY 64 QNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
DQ 202 QNSTFRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTIKTK 247

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RESULT 12

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Q6N030 PRELIMINARY; PRT; 518 AA.
AC Q6N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I15212.
GN Name=DKFZp686I15212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Meves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match          91.2%; Score 529; DB 2; Length 518;
Best Local Similarity 92.5%; Pred. No. 1.9e-44;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 306 LGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 365
QY 64 QNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
DQ 366 QNSTFRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTIKTK 411

RESULT 13
GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Meves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match          91.2%; Score 529; DB 2; Length 518;
Best Local Similarity 92.5%; Pred. No. 1.9e-44;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 306 LGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 365
QY 64 QNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
DQ 366 QNSTFRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTIKTK 411

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RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; [Biochemistry](#) 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; [Biochemistry](#) 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure."; [Hoppe-Seyler's Z. Physiol. Chem.](#) 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; [Hoppe-Seyler's Z. Physiol. Chem.](#) 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."; [Biochemistry](#) 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges."; [Hoppe-Seyler's Z. Physiol. Chem.](#) 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from *Staphylococcus*
RT aureus at 2.9- and 2.8-A resolution."; [Biochemistry](#) 20:2361-2370(1981).
RN [9]
CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A93433; GHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1D5B; X-ray; B/H=1-101.
DR PDB; 1D5I; X-ray; H=1-101.
DR PDB; 1D6V; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-329.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1H2H; X-ray; H/K=1-330.
DR PDB; 1I7Z; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1LOX; X-ray; A/B=119-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; .
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0008955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS05835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83 Interchain (with light chain).
FT DISULFID 103 103 Interchain (with heavy chain).
FT DISULFID 109 109 Interchain (with heavy chain).
FT DISULFID 112 112 Interchain (with heavy chain).
FT DISULFID 144 204 N-linked (GlcNAc. . .).
FT DISULFID 250 308 K -> R (in G1M(3) marker).
FT CARBOHYD 180 180 /FTID=VAR_003886.
FT VARIANT 97 97 D -> E (in G1M(non-1) marker).
FT VARIANT 239 239 /FTID=VAR_003887.
FT VARIANT 241 241 L -> M (in G1M(non-1) marker).
FT VARIANT 241 241 /FTID=VAR_003888.
FT STRAND 23 24
FT STRAND 26 33
FT STRAND 38 38
FT STRAND 41 41
FT TURN 42 45
FT TURN 48 49
FT STRAND 50 52
FT STRAND 57 58
FT TURN 59 61
FT STRAND 62 71
FT HELIX 73 75
FT TURN 76 78
FT STRAND 82 87
FT TURN 88 91
FT STRAND 92 97
FT TURN 102 103
FT STRAND 122 126
FT TURN 130 134
FT TURN 136 137
FT STRAND 141 149
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 167
FT STRAND 171 171

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FT STRAND 176 177
FT TURN 179 180
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
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FT STRAND 274 276
FT STRAND 280 281
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FT STRAND 287 296
FT HELIX 297 301
FT STRAND 302 303
FT STRAND 306 311
FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 90.3%; Score 524; DB 1; Length 330;
Best Local Similarity 86.0%; Pred. No. 3.6e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVGVHN 55
Db 110 PPCAPELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVGVHN 169

QY 56 AKTKPREEQFNSTRFVSVLTVVHQDVLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 170 AKTKPREEQYNSTRFVSVLTVVHQDVLNGKEYCKVSNKGLPSSIEKTIISKTK 223

RESULT 14
Q6PYX1
ID Q6PYX1 PRELIMINARY; PRT; 348 AA.
AC Q6PYX1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalusz D., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 90.3%; Score 524; DB 2; Length 465;
Best Local Similarity 86.0%; Pred. No. 5.3e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVGVHN 55
Db 110 PPCAPELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVGVHN 169

QY 56 AKTKPREEQFNSTRFVSVLTVVHQDVLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 170 AKTKPREEQYNSTRFVSVLTVVHQDVLNGKEYCKVSNKGLPSSIEKTIISKTK 223

RESULT 15
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ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalusz D., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 90.3%; Score 524; DB 2; Length 465;
Best Local Similarity 86.0%; Pred. No. 5.3e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVGVHN 55
Db 110 PPCAPELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVGVHN 169

QY 56 AKTKPREEQFNSTRFVSVLTVVHQDVLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 170 AKTKPREEQYNSTRFVSVLTVVHQDVLNGKEYCKVSNKGLPSSIEKTIISKTK 223

RESULT 16
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ID Q6PYX1 PRELIMINARY; PRT; 348 AA.
AC Q6PYX1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY570731; AAS88328.1; -.
DR HSP; P01857; IAU7.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS0835; IG LIKE; 3.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Receptor.
FT NON_TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0BES845 CRC64;

Query Match 90.3%; Score 524; DB 2; Length 348;
Best Local Similarity 86.0%; Pred. No. 3.8e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;
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Db 245 PPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 304

Qy 56 AKTKPREQFNSTFRVSVLTVVHQDLNKGKEYKCKVSNKGLPSSIEKTIISKTK 109

Db 305 AKTKPREQVNSTYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISRKA 358

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Job time : 79.8836 secs

Nov 17 11:27:19 2005

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.3881 Seconds
(without alignments)
333.636 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	99.5	448	4	US-09-968-362A-18
2	572	98.6	109	3	US-08-444-644-30
3	572	98.6	109	3	US-08-232-246A-30
4	572	98.6	217	4	US-09-483-588-5
5	572	98.6	228	4	US-09-968-362A-27
6	572	98.6	432	3	US-08-477-460B-2
7	572	98.6	432	3	US-08-379-516-2
8	572	98.6	432	3	US-09-329-916-2
9	572	98.6	432	3	US-08-485-372A-2
10	572	98.6	432	3	US-09-409-006A-2
11	572	98.6	432	4	US-08-484-681-2
12	572	98.6	432	4	US-09-766-995-2
13	572	98.6	432	5	PCT-US93-07422-2
14	572	98.6	451	4	US-09-472-087-70
15	572	98.6	463	4	US-09-472-087-1
16	572	98.6	463	4	US-09-472-087-4
17	572	98.6	463	4	US-09-472-087-63
18	572	98.6	463	4	US-09-472-087-68
19	572	98.6	464	4	US-09-472-087-2
20	572	98.6	464	4	US-09-472-087-66
21	572	98.6	470	4	US-09-859-053-28
22	572	98.6	470	4	US-09-859-053-32
23	572	98.6	470	4	US-09-859-053-36
24	572	98.6	530	3	US-08-477-460B-4
25	572	98.6	530	3	US-08-379-516-4
26	572	98.6	530	3	US-09-329-916-4
27	572	98.6	530	3	US-08-485-372A-4

28	572	98.6	530	3	US-09-409-006A-4	Sequence 4, Appli
29	572	98.6	530	4	US-08-484-681-4	Sequence 4, Appli
30	572	98.6	530	4	US-09-766-995-4	Sequence 4, Appli
31	572	98.6	530	5	PCT-US93-07422-4	Sequence 4, Appli
32	569	98.1	450	2	US-08-788-800-12	Sequence 12, Appl
33	569	98.1	469	2	US-07-934-373C-23	Sequence 23, Appl
34	569	98.1	469	3	US-08-437-642B-23	Sequence 23, Appl
35	569	98.1	469	4	US-08-146-206C-23	Sequence 23, Appl
36	569	98.1	469	4	US-09-705-686-23	Sequence 23, Appl
37	569	98.1	469	4	US-09-705-392A-23	Sequence 23, Appl
38	569	98.1	469	4	US-09-705-398-23	Sequence 23, Appl
39	569	98.1	552	5	PCT-US93-07832-23	Sequence 23, Appl
40	566	97.6	463	4	US-09-472-087-64	Sequence 64, Appl
41	562	96.9	326	2	US-08-656-586-9	Sequence 9, Appli
42	562	96.9	462	4	US-09-627-896B-24	Sequence 24, Appl
43	537.5	92.7	449	4	US-09-968-362A-20	Sequence 20, Appl
44	536	92.4	109	2	US-08-070-116A-4	Sequence 4, Appli
45	536	92.4	109	4	US-08-557-050-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-968-362A-18
; Sequence 18, Application US/09968362A

; Patent No. 6797493

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor

; FILE OF INVENTION: increased biological activities

; FILE REFERENCE: 03SUN2001

; CURRENT APPLICATION NUMBER: US/09/968.362A

; CURRENT FILING DATE: 2001-10-01

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 18

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: hG-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure

; OTHER INFORMATION: 2A)

US-09-968-362A-18

Query Match 99.5%; Score 577; DB 4; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.7e-59;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	APPVAGPSVFLFPKPKDTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVVHNATKTP	60
Db	233	APPVAGPSVFLFPKPKDTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVVHNATKTP	292
Qy	61	RESEQNSTFRVSVLTIVVHQDLNKGKEYCKVSNKGLPSSIEKTIKTK	109
Db	293	RESEQNSTFRVSVLTIVVHQDLNKGKEYCKVSNKGLPASTIEKTIKTK	341

RESULT 2

US-08-444-644-30
; Sequence 30, Application US/08444644

; Patent No. 6015555

; GENERAL INFORMATION:

; APPLICANT: Friden, Phillip M.

; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

; TITLE OF INVENTION: CONJUGATES

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

```
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/444,644
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1989
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAZ
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match          98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPAPIEKTIKTK 109

RESULT 3
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/232,246A
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-30

Query Match          98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPAPIEKTIKTK 109

RESULT 4
US-09-483-588-5
; Sequence 5, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/09/483,588
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: US 60/116,023
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-483-588-5

Query Match          98.6%; Score 572; DB 4; Length 217;
Best Local Similarity 98.2%; Pred. No. 4.1e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
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Db 62 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 110
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RESULT 5
US-09-968-362A-27
; Sequence 27, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Human IgG2 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-27

Query Match 98.6%; Score 572; DB 4; Length 228;
Best Local Similarity 98.2%; Pred. No. 4.4e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 13 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 72
Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 73 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 121

RESULT 6
US-08-477-460B-2
; Sequence 2, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
```

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; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276
Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 277 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 7
US-08-379-516-2
; Sequence 2, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; FILE REFERENCE: Immunoconjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276
Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 277 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 8
US-09-329-916-2
; Sequence 2, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
```

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;
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,460
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-09-329-916-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276

QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 277 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTK 325

US-09-329-916-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276

QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 277 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTK 325

US-09-329-916-2

RESULT 9
US-08-485-372A-2
; Sequence 2, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE: 07-AUG-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

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; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-08-485-372A-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276

QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 277 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTK 325

US-08-485-372A-2

RESULT 10
US-09-409-006A-2
; Sequence 2, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,006A
; FILING DATE: 29-SEP-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-409-006A-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
Qy 61 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIISKTK 109
Db 277 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 11

US-08-484-681-2
Sequence 2, Application US/08484681
Patent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-484-681-2

Query Match 98.6%; Score 572; DB 4; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
Qy 61 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIISKTK 109
Db 277 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 12

US-09-766-995-2
Sequence 2, Application US/09766995
Patent No. 6737267
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: homo sapiens
US-09-766-995-2

Query Match 98.6%; Score 572; DB 4; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
Qy 61 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIISKTK 109
Db 277 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 13

PCT-US93-07422-2
Sequence 2, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA: US 07/927,931
FILING DATE: 07-AUG-1992

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; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPH/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; PCT-US93-07422-2

Query Match      98.6%; Score 572; DB 5; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276

Qy 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTIKTK 325

RESULT 14
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-70

Query Match      98.6%; Score 572; DB 4; Length 451;
Best Local Similarity 98.2%; Pred. No. 1.1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 236 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 295

Qy 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 296 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTIKTK 344
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RESULT 15

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US-09-472-087-1
; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-1

Query Match      98.6%; Score 572; DB 4; Length 463;
Best Local Similarity 98.2%; Pred. No. 1.1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 248 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 307

Qy 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 308 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTIKTK 356

Search completed: November 17, 2005, 07:13:21
Job time : 25.3881 sec
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 83.6164 Seconds
(without alignments)
545.427 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGSVFLFPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	580	100.0	447	16 US-10-745-775-16	Sequence 16, Appl
2	577	99.5	436	10 US-09-932-812-18	Sequence 18, Appl
3	577	99.5	436	16 US-10-761-593A-18	Sequence 18, Appl
4	577	99.5	436	20 US-11-016-518A-18	Sequence 18, Appl
5	577	99.5	436	20 US-11-017-185-18	Sequence 18, Appl
6	577	99.5	448	10 US-09-968-362-18	Sequence 18, Appl
7	577	99.5	448	16 US-10-800-497-18	Sequence 18, Appl
8	577	99.5	448	16 US-10-800-449-18	Sequence 18, Appl
9	572	98.6	109	18 US-10-959-318-2	Sequence 2, Appl
10	572	98.6	217	9 US-09-813-341-3	Sequence 3, Appl
11	572	98.6	217	14 US-10-277-370-3	Sequence 3, Appl

12	572	98.6	217	14	US-10-196-394-74	Sequence 74, Appl
13	572	98.6	217	15	US-10-370-749-16	Sequence 16, Appl
14	572	98.6	217	16	US-10-835-642-5	Sequence 5, Appl
15	572	98.6	217	16	US-10-757-863-5	Sequence 5, Appl
16	572	98.6	217	17	US-10-982-470-5	Sequence 5, Appl
17	572	98.6	217	20	US-11-158-839-5	Sequence 5, Appl
18	572	98.6	228	15	US-10-466-593-3	Sequence 3, Appl
19	572	98.6	228	16	US-10-761-593A-27	Sequence 27, Appl
20	572	98.6	228	16	US-10-800-449-27	Sequence 27, Appl
21	572	98.6	228	16	US-10-800-449-27	Sequence 27, Appl
22	572	98.6	228	20	US-11-016-518A-27	Sequence 27, Appl
23	572	98.6	228	20	US-11-017-185-27	Sequence 27, Appl
24	572	98.6	310	16	US-10-684-109-75	Sequence 75, Appl
25	572	98.6	326	13	US-10-047-542-22	Sequence 22, Appl
26	572	98.6	326	14	US-10-310-719-9	Sequence 9, Appl
27	572	98.6	326	14	US-10-112-582-2	Sequence 2, Appl
28	572	98.6	326	15	US-10-038-591-28	Sequence 28, Appl
29	572	98.6	326	15	US-10-656-769-6	Sequence 6, Appl
30	572	98.6	326	16	US-10-775-444A-28	Sequence 28, Appl
31	572	98.6	326	16	US-10-756-153-32	Sequence 32, Appl
32	572	98.6	326	17	US-10-872-932A-37	Sequence 37, Appl
33	572	98.6	326	17	US-10-928-305-8	Sequence 8, Appl
34	572	98.6	326	17	US-10-891-658-4	Sequence 4, Appl
35	572	98.6	326	17	US-10-893-576-46	Sequence 46, Appl
36	572	98.6	326	18	US-10-810-881A-36	Sequence 36, Appl
37	572	98.6	326	18	US-10-981-936-36	Sequence 36, Appl
38	572	98.6	326	20	US-11-001-980-2	Sequence 2, Appl
39	572	98.6	326	20	US-11-001-980-6	Sequence 6, Appl
40	572	98.6	326	20	US-11-004-054-4	Sequence 4, Appl
41	572	98.6	326	20	US-11-026-998-23	Sequence 23, Appl
42	572	98.6	326	20	US-11-027-309A-23	Sequence 23, Appl
43	572	98.6	432	8	US-08-485-163-3	Sequence 3, Appl
44	572	98.6	432	9	US-09-766-995-2	Sequence 2, Appl
45	572	98.6	442	20	US-11-034-655-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-745-775-16
; Sequence 16, Application US/10745775
; Publication No. US20040237124A1
; GENERAL INFORMATION:
; APPLICANT: Pons, Jaume
; APPLICANT: Rosenthal, Arnon
; TITLE OF INVENTION: ANTI-NGF ANTIBODIES AND METHODS USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514712001400
; CURRENT APPLICATION NUMBER: US/10745,775
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/436,905
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 60/443,522
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/510,006
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16,
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-745-775-16

Query Match 100.0%; Score 580; DB 16; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDTLMIKRTPEVTCTVAVDVSHEDPEVQFNWYVDGVVEHNATKPK 60
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Db 232 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 291

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 109
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Db 292 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 340
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RESULT 2

US-09-932-812-18

; Sequence 18, Application US/09932812

; Publication No. US2003008749A1

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity

; FILE REFERENCE: 02SUN2001

; CURRENT APPLICATION NUMBER: US/09/932,812

; CURRENT FILING DATE: 2001-10-30

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)

US-09-932-812-18

Query Match 99.5%; Score 577; DB 10; Length 436;

Best Local Similarity 99.1%; Pred. No. 2.4e-48;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
|||||

Db 221 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 280
|||||

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 109
|||||

Db 281 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 329
|||||

RESULT 3

US-10-761-593A-18

; Sequence 18, Application US/10761593A

; Publication No. US20040175824A1

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological activity

; FILE REFERENCE: 02SUN2001-A

; CURRENT APPLICATION NUMBER: US/10/761,593A

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: 09/932812

; PRIOR FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 18

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)

US-10-761-593A-18

Query Match 99.5%; Score 577; DB 16; Length 436;

Best Local Similarity 99.1%; Pred. No. 2.4e-48;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Db 221 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 280
|||||

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 109
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Db 281 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 329
|||||

RESULT 4

US-11-016-518A-18

; Sequence 18, Application US/11016518A

; Publication No. US20050124045A1

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity

; FILE REFERENCE: 02SUN2004D1

; CURRENT APPLICATION NUMBER: US/11/016,518A

; CURRENT FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: US 09/932,812

; PRIOR FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 18

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)

US-11-016-518A-18

Query Match 99.5%; Score 577; DB 20; Length 436;

Best Local Similarity 99.1%; Pred. No. 2.4e-48;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Db 221 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 280
|||||

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 109
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Db 281 REEQFNSTFRVSVLTVVHQDNLNGKEYCKCKVSNKGLPSSIEKTIISKTK 329
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RESULT 5

US-11-017-185-18

; Sequence 18, Application US/11017185

; Publication No. US20050142642A1

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity

; FILE REFERENCE: 02SUN2001D2

; CURRENT APPLICATION NUMBER: US/11/017,185

; CURRENT FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: US 09/932,812

; PRIOR FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)

US-11-017-185-18

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Query Match      99.5%; Score 577; DB 20; Length 436;
Best Local Similarity 99.1%; Pred. No. 2.4e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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Db 221 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 280

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 281 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 329

RESULT 6
US-09-968-362-18
; Sequence 18, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-09-968-362-18

Query Match      99.5%; Score 577; DB 10; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
    |||||
Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 7
US-10-800-497-18
; Sequence 18, Application US/10800497
; Publication No. US2004025209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; TITLE OF INVENTION: stimulaing factor with
; FILE REFERENCE: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-09-968-362-18

Query Match      99.5%; Score 577; DB 10; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 8
US-10-800-449-18
; Sequence 18, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-449-18

Query Match      99.5%; Score 577; DB 16; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
    |||||
Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 9
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215769A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-497-18
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; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader
; OTHER INFORMATION: peptide (Figure
; OTHER INFORMATION: 2A)
US-10-800-497-18

Query Match      99.5%; Score 577; DB 16; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
    |||||
Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 8
US-10-800-449-18
; Sequence 18, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-449-18

Query Match      99.5%; Score 577; DB 16; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 9
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215769A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-497-18
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-2

Query Match      98.6%; Score 572; DB 18; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.6e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIETIKTK 109

RESULT 10
US-09-813-341-3
; Sequence 3, Application US/09813341
; Publication No. US20020004587A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Kathy L.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
; FILE REFERENCE: P1780R1
; CURRENT FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-341-3

Query Match      98.6%; Score 572; DB 9; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIETIKTK 110

RESULT 11
US-10-277-370-3
; Sequence 3, Application US/10277370
; Publication No. US20030157108A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Glycoprotein Compositions
; FILE REFERENCE: P1877R1
; CURRENT APPLICATION NUMBER: US/10/277,370
; CURRENT FILING DATE: 2003-02-10
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/347,694
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens

US-10-277-370-3
; Sequence 16, Application US/10370749
; Publication No. US20040002587A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Allan, Barrett
; TITLE OF INVENTION: FC Region Variants
; FILE REFERENCE: AME-07823
; CURRENT APPLICATION NUMBER: US/10/370,749
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/358,161
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-370-749-16

Query Match      98.6%; Score 572; DB 15; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIETIKTK 110

RESULT 12
US-10-196-394-74
; Sequence 74, Application US/10196394
; Publication No. US20030171278A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Compounds that Bind HER2
; FILE REFERENCE: P1713R1
; CURRENT APPLICATION NUMBER: US/10/196,394
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US/09/609,721
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/142,232
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 74
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-196-394-74

Query Match      98.6%; Score 572; DB 14; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIETIKTK 110

RESULT 13
US-10-370-749-16
; Sequence 16, Application US/10370749
; Publication No. US20040002587A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Allan, Barrett
; TITLE OF INVENTION: FC Region Variants
; FILE REFERENCE: AME-07823
; CURRENT APPLICATION NUMBER: US/10/370,749
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/358,161
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-370-749-16

Query Match      98.6%; Score 572; DB 15; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 61
Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 110

RESULT 14
US-10-835-642-5
; Sequence 5, Application US/10835642
; Publication No. US20040191244A1
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/10/835,642
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/483,588
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/116,023
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-835-642-5

Query Match 98.6%; Score 572; DB 16; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 61
Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 110

RESULT 15
US-10-757-863-5
; Sequence 5, Application US/10757863
; Publication No. US20040228856A1
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/10/757,863
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/483,588
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/116,023
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-757-863-5

Query Match 98.6%; Score 572; DB 16; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 61

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 110
Search completed: November 17, 2005, 07:37:35
Job time : 84.6164 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.0913 Seconds
(without alignments)
473.187 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGSVFLFPKPKDTL.....CKVSNKGLPSSIKTKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	98.6	109	2	AAR41709 Undefined
2	572	98.6	109	3	AAY54997 Mutated C
3	562	96.9	109	3	AAY54996 Mutated C
4	540.5	93.2	110	3	AAY54998 Mutated C
5	536	92.4	109	2	AAR67438 OKT3 mono
6	536	92.4	110	2	AAR41717 Undefined
7	523	90.2	109	7	Add25659 Binding d
8	523	90.2	110	2	AAR27680 Human imm
9	523	90.2	110	2	AAR41684 Undefined
10	523	90.2	110	8	ADH75385 Human IgG
11	522	90.0	102	8	ADJ52132 CHI delet
12	522	90.0	105	2	AAY42626 Human IgG
13	518	89.3	109	5	AAE28089 Human imm
14	518	89.3	110	8	ADH75415 CH2 regio
15	517	89.1	110	8	ADL90103 Human imm
16	516	89.0	110	8	ADH75413 CH2 regio
17	515	88.8	109	7	Add25761 Binding d
18	514	88.6	110	2	AAR41713 Undefined
19	509	87.8	102	8	ADJ52129 CHI Delet
20	408	70.3	110	2	AAW71023 Mus muscu
21	383	66.0	110	1	AAP83207 Sequence
22	347	59.8	72	8	ADL15711 Human imm
23	321	55.3	66	2	AAR75349 C-gamma-1
24	321	55.3	66	2	AAR75351 C-gamma-1
25	309	53.3	76	8	ADL15713 Human imm

26	274	47.2	56	1	AAP83205 Sequence
27	273.5	47.2	56	1	AAP83204 Sequence
28	270	46.6	56	1	AAP83201 Sequence
29	270	46.6	56	1	AAP83202 Sequence
30	269.5	46.5	56	1	AAP83203 Sequence
31	268.5	46.3	56	1	AAP83206 Sequence
32	247	42.6	46	8	ADR59139 Human IgG
33	238.5	41.1	110	2	AAR33315 Variant I
34	234	40.3	46	8	ADR59138 Human IgG
35	219	37.8	46	8	ADR59143 Rhesus mo
36	217	37.4	46	8	ADR59142 Rhesus mo
37	209.5	36.1	110	2	AAR33314 Variant I
38	203.5	35.1	110	2	AAR33316 Variant I
39	199.5	34.4	110	2	AAR33693 Variant I
40	199	34.3	96	3	AAB53640 Human col
41	198	34.1	46	8	ADR59140 Rhesus mo
42	198	34.1	46	8	ADR59141 Crab-eati
43	197	34.0	46	8	ADR59145 Pig IGG2a
44	197	34.0	46	8	ADR59148 Camel I9G
45	192.5	33.2	110	2	AAR33318 Variant I

ALIGNMENTS

RESULT 1
AAR41709
ID AAR41709 standard; protein; 109 AA.
XX
AC AAR41709;
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
DE Undefined ORF2 encoded by plasmid pAH4625.

KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
OS Synthetic.
XX
PN WO9310819-A1.
XX
PD 10-JUN-1993.

XX 24-NOV-1992; 92WO-US010206.
XX
PR 26-NOV-1991; 91US-00800458.
XX
PA (ALKE-) ALKERMES INC.

XX Friden PM;
XX WPI; 1993-196742/24.
XX N-PSDB; AAQ43846.

PT Antibody conjugates specific for transferrin receptor - used for
diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
PS Disclosure; Fig 17J; 151pp; English.

CC The sequences given in AAR41707-09 are encoded by the expression vector
pAH4625. This vector represents the cloning of the human gamma isotype,
gamma-2, with the variable region of the murine monoclonal antibody
128.1. This plasmid encodes a chimeric monoclonal antibody in which the
heavy chain (VH) is derived from a murine source and the sequences
encoding CH1, CH2 and CH3 are derived from a human source. This vector,
in combination with the chimeric light chain vector, pAQ4611 (see also
AAQ43845), was transfected into SP2/0 cells and clones were isolated.

CC 128.1 is an anti-human transferrin receptor antibody which binds to the
CC transferrin receptor on brain capillary endothelial cells. This antibody
CC may be used in a conjugate in which it is linked to a neuropharmaceutical
CC or diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 109 AA;

Query Match 98.6%; Score 572; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
DB 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPAPIETIKTK 109

RESULT 2
AAV54997
ID AAV54997 standard; protein; 109 AA.
XX
AC AAV54997;
XX
DT 17-FEB-2000 (first entry)
DE Mutated CH2 sequence G2deltaaa.
XX
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
OS Synthetic.
XX
PN WO9558572-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB001441.
XX
PR 08-MAY-1998; 98GB-00009951.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Armour KL, Clark MR, Williamson LM;
XX
DR WPI; 2000-039075/03.
XX
PT Immunoglobulin-derived binding molecules that do not activate complement
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
PT properties.
XX
PS Claim 12; Fig 17; 81pp; English.
XX
CC This sequence represents the mutated CH2 molecule G2deltaaa, and is a
CC binding molecule of the invention. The recombinant binding molecule is
CC capable of binding a target molecule without triggering complement
CC dependent lysis, or the cell-mediated destruction of the target
CC comprises: (a) a binding domain capable of binding a target molecule; and
CC (b) an effector domain that is homologous to all or part of a constant
CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC molecule is used to bind a target molecule (especially FcgammaRIIb

CC causing inhibition of B cell activation, mast cell degranulation or
CC phagocytosis). The binding molecule can be used to prevent or inhibit the
CC binding of a second binding molecule, e.g. an antibody, to the target
CC molecule. The binding molecule is useful for the treatment of graft-vs-
CC host disease, organ transplant rejection, bone-marrow transplant
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC coronary artery occlusion). The binding molecules do not activate
CC complement or trigger cytotoxic activities through FcgammaRIIb and desirable
CC IgG properties have been retained. The polypeptides do not contain non-
CC human amino acids, and are therefore likely to have reduced
CC immunogenicity. Further, they still bind Protein A, which is consistent
CC with being able to cross the human placenta through interaction with FcRn
CC (neonatal Fc receptor)
XX
SQ Sequence 109 AA;

Query Match 98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 99.1%; Pred. No. 1.6e-50;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
DB 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 3
AAV54996
ID AAV54996 standard; protein; 109 AA.
XX
AC AAV54996;
XX
DT 17-FEB-2000 (first entry)
DE Mutated CH2 sequence G1deltaab.
XX
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
OS Synthetic.
XX
PN WO9558572-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB001441.
XX
PR 08-MAY-1998; 98GB-00009951.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Armour KL, Clark MR, Williamson LM;
XX
DR WPI; 2000-039075/03.
XX
PT Immunoglobulin-derived binding molecules that do not activate complement
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
PT properties.
XX


```

PS  Claim 12; Fig 17; 81pp; English.
XX
XX  This sequence represents the mutated CH2 molecule G1deltaaac, and is a
CC  binding molecule of the invention. The recombinant binding molecule is
CC  capable of binding a target molecule without triggering complement
CC  dependent lysis, or the cell-mediated destruction of the target
CC  comprises: (a) a binding domain capable of binding a target molecule; and
CC  (b) an effector domain that is homologous to all or part of a constant
CC  domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC  molecule is used to bind a target molecule (especially FcgammaRIIb
CC  causing inhibition of B cell activation, mast cell degranulation or
CC  phagocytosis). The binding molecule can be used to prevent or inhibit the
CC  binding of a second binding molecule, e.g. an antibody, to the target
CC  molecule. The binding molecule is useful for the treatment of graft-vs-
CC  host disease, organ transplant rejection, bone-marrow transplant
CC  rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC  autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
CC  foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
CC  chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC  (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC  coronary artery occlusion). The binding molecules do not activate
CC  complement or trigger cytotoxic activities through FcgammaRIIb and desirable
CC  IgG properties have been retained. The polypeptides do not contain non-
CC  human amino acids, and are therefore likely to have reduced
CC  immunogenicity. Further, they still bind Protein A, which is consistent
CC  with being able to cross the human placenta through interaction with FcRn
CC  (neonatal Fc receptor)
XX
SQ  Sequence 109 AA;
Query Match          96.9%; Score 562; DB 3; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.7e-49;
Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY  1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
DB  1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY  61 REEQFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPSSIEKTIKTK 109
DB  61 REEQYNSTYRVSVLTVLHQDNLNGKEYKCKVSNKGLPSSIEKTIKSKAK 109
RESULT 4
ID  AAY54998 standard; protein; 110 AA.
XX  AAY54998;
XX
XX  17-FEB-2000 (first entry)
XX
XX  Mutated CH2 sequence G1deltaaac.
XX
KW  Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW  cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW  B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW  Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW  bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW  autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW  autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW  neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
KW  sickle cell anaemia; coronary artery occlusion.
XX
OS  Synthetic.
XX
XX  WO9958572-A1.
XX
XX  18-NOV-1999.
XX
XX  07-MAY-1999; 99WO-GB001441.
XX
XX  08-MAY-1998; 98GB-00009951.
XX
XX

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PA  (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX  Armour KL, Clark MR, Williamson LM;
XX
XX  WPI; 2000-039075/03.
XX
XX  Immunoglobulin-derived binding molecules that do not activate complement
XX  or trigger cytotoxic activities and maintaining desirable immunoglobulin
XX  properties.
XX
XX  Claim 12; Fig 17; 81pp; English.
XX
XX  This sequence represents the mutated CH2 molecule G1deltaaac, and is a
CC  binding molecule of the invention. The recombinant binding molecule is
CC  capable of binding a target molecule without triggering complement
CC  dependent lysis, or the cell-mediated destruction of the target
CC  comprises: (a) a binding domain capable of binding a target molecule; and
CC  (b) an effector domain that is homologous to all or part of a constant
CC  domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC  molecule is used to bind a target molecule (especially FcgammaRIIb
CC  causing inhibition of B cell activation, mast cell degranulation or
CC  phagocytosis). The binding molecule can be used to prevent or inhibit the
CC  binding of a second binding molecule, e.g. an antibody, to the target
CC  molecule. The binding molecule is useful for the treatment of graft-vs-
CC  host disease, organ transplant rejection, bone-marrow transplant
CC  rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC  autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
CC  foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
CC  chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC  (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC  coronary artery occlusion). The binding molecules do not activate
CC  complement or trigger cytotoxic activities through FcgammaRIIb and desirable
CC  IgG properties have been retained. The polypeptides do not contain non-
CC  human amino acids, and are therefore likely to have reduced
CC  immunogenicity. Further, they still bind Protein A, which is consistent
CC  with being able to cross the human placenta through interaction with FcRn
CC  (neonatal Fc receptor)
XX
SQ  Sequence 110 AA;
Query Match          93.2%; Score 540.5; DB 3; Length 110;
Best Local Similarity 93.6%; Pred. No. 2.7e-47;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
QY  1 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
DB  1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY  60 PREEQFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPSSIEKTIKTK 109
DB  61 PREEQYNSTYRVSVLTVLHQDNLNGKEYKCKVSNKGLPSSIEKTIKSKAK 110
RESULT 5
AAR67438
ID  AAR67438 standard; protein; 109 AA.
XX  AAR67438;
XX
XX  25-MAR-2003 (revised)
XX  08-JUL-1995 (first entry)
XX
XX  OKT3 monoclonal antibody fragment.
XX
XX  OKT3; monoclonal antibody; antibody engineering; immunosuppressive;
XX  humanized antibody.
XX
XX  Mus musculus.
XX
XX  WO9428027-A1.
XX
XX  08-DEC-1994.
XX

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PF 01-JUN-1994; 94WO-US06198.
XX
PR 01-JUN-1993; 93US-00070116.
XX
PA (ARCH-) ARCH DEV CORP.
XX
XX Bluestone JA, Zivin RA, Jolliffe L;
PI
XX WPI; 1995-022721/03.
XX
DR P-PSDB; AAQ75356.
XX
XX New humanised OKT3 antibody with mutated Fc receptor binding region -
PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
PT cell activating side effects of wild type antibody.
XX
XX Disclosure; Page 82-87; 135pp; English.
XX
CC The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-
CC cell activating and immunosuppressive activity, and is used to treat
CC transplant patients to prevent rejection. The antibody can be engineered
CC to contain a human Fc region. By transferring the binding specificity
CC into a human framework, the immunogenicity is reduced without affecting
CC the immunosuppressive activity. (Updated on 25-MAR-2003 to correct FN
CC field.)
XX
SQ Sequence 109 AA;
Query Match 92.4%; Score 536; DB 2; Length 109;
Best Local Similarity 94.3%; Pred. No. 7.6e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63
QY 64 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 110
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 6
AAR41717
ID AAR41717 standard; protein; 110 AA.
XX
XX AAR41717;
AC
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
XX Undefined ORF2 encoded by plasmid pAH4808.
XX
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
XX light; chain; variable; constant; region; anti-human; pAH4807;
XX transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
XX endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
XX diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
XX Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
XX Synthetic.
OS
XX
XX WO9310819-A1.
PN
XX
XX 10-JUN-1993.
XX
XX 24-NOV-1992; 92WO-US010206.
XX
XX 26-NOV-1991; 91US-00800458.
PR
XX (ALKE-) ALKERMES INC.
PA
XX Friden PM;
PI
XX WPI; 1993-196742/24.
DR

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DR N-PSDB; AAQ43848.
XX
XX Antibody conjugates specific for transferrin receptor - used for
PT diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
XX Disclosure; Fig 19J; 151pp; English.
XX
XX The sequences given in AAR41715-18 are encoded by the expression vector
CC pAH4808. This vector represents the cloning of the human gamma isotype,
CC gamma-4, with the variable region of the murine monoclonal antibody
CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the
CC heavy chain (VH) is derived from a murine source and the sequences
CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,
CC in combination with the chimeric light chain vector, pAG4611 (see also
CC AAQ43845), was transfected into SP2/0 cells and clones were isolated
CC 128.1 is an anti-human transferrin receptor antibody which binds to the
CC transferrin receptor on brain capillary endothelial cells. This antibody
CC may be used in a conjugate in which it is linked to a neuropharmaceutical
CC or diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods. (Updated on 25-MAR-2003 to correct FN field.)
XX
XX Sequence 110 AA;
Query Match 92.4%; Score 536; DB 2; Length 110;
Best Local Similarity 94.3%; Pred. No. 7.7e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 64
QY 64 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 110
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 7
ADD25659
ID ADD25659 standard; protein; 109 AA.
XX
XX ADD25659;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Binding domain-immunoglobulin fusion protein-associated protein #107.
DE
XX
XX Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
XX Unidentified.
OS
XX
XX US2003118592-A1.
PN
XX
XX 26-JUN-2003.
PD
XX
XX 25-JUL-2002; 2002US-00207655.
PF
XX 17-JAN-2001; 2001US-0367358P.
PR
XX 17-JAN-2002; 2002US-0005350.
PR
XX 03-JUN-2002; 2002US-0385691P.
PR
XX (GENE-) GENE-CRAFT INC.
PA
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
PI
XX

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DR WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a

PT subject having or suspected of having a malignant condition or a B-cell

PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

XX

XX Disclosure; SEQ ID NO 220; 157pp; English.

PS

CC The invention relates to a binding domain-immunoglobulin fusion protein

CC comprising a binding domain polypeptide that is fused to an

CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain

CC CH2 constant region polypeptide that is fused to the hinge region

CC polypeptide, and an immunoglobulin heavy chain CH3 constant region

CC polypeptide that is fused to the CH2 constant region polypeptide. The

CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin

CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge

CC region polypeptide; derived from (a) having 3 or more cysteine residues;

CC where the mutated human IgG1 immunoglobulin hinge region polypeptide

CC contains 2 cysteine residues, where the first cysteine is not mutated; a

CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from

CC (a) having 3 or more cysteine residues, where the mutated human IgG1

CC immunoglobulin hinge region polypeptide contains no more than one

CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region

CC polypeptide, derived from (a) having 3 or more cysteine residues; where

CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains

CC no cysteine residues. The binding domain-immunoglobulin fusion protein is

CC capable of at least one immunological activity comprising antibody

CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The

CC binding domain polypeptide is capable of specifically binding to an

CC antigen. Also included are an isolated polynucleotide encoding the

CC binding domain-immunoglobulin fusion protein, a recombinant expression

CC construct comprising the polynucleotide (operably linked to a promoter),

CC a host cell transformed or transfected with a recombinant expression

CC construct, producing the binding domain-immunoglobulin fusion protein, a

CC pharmaceutical composition comprising the binding domain-immunoglobulin

CC fusion protein or polynucleotide and a carrier, and treating a subject

CC having or suspected of having a malignant condition or a B-cell disorder.

CC The binding domain-immunoglobulin fusion protein is useful for treating a

CC subject having or suspected of having a malignant condition or a B-cell

CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,

CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple

CC sclerosis or autoimmune disease. The present sequence is a binding domain

CC -immunoglobulin fusion protein-associated protein sequence. Note: The

CC sequence data for this patent formed part of the printed specification

CC and is also available in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not

CC identified the sequences in the printed specification by their SEQ ID

CC number therefore none of the sequences can be explicitly identified.

XX

SQ Sequence 109 AA;

Query Match 90.2%; Score 523; DB 7; Length 109;

Best Local Similarity 90.6%; Pred. No. 1.6e-45;

Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 4 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 64

Qy 64 QFNSTFRVSVLTIVVHODWLNKKEYCKVSKNGKLPSSIEKTIKTK 109

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 64 QYNSTYRWVSVLTVLHODWLNKKEYCKVSKNGKLPAPIEKTISKAK 110

RESULT 8

AAR27680

ID AAR27680 standard; protein; 110 AA.

XX

XX AAR27680;

XX

XX 25-MAR-2003 (revised)

DT 10-MAR-1993 (first entry)

XX

DE Human immunoglobulin IgG1 CH2 region.

XX Isoallotype; IgG1 G1m(1,2,17); anti-allotype response; humanised Ab.

XX Homo sapiens.

OS

XX WO9216562-A1.

PN

XX 01-OCT-1992.

PD

XX 12-MAR-1992; 92WO-GB000445.

PF

XX 12-MAR-1991; 91GB-00005245.

PR

XX (LYNX-) LYNXVALE LTD.

PA

XX Clark MR;

PI

XX WPI; 1992-349162/42.

DR

XX Humanised antibodies having modified allotypic determinant - useful for

PT matching allotypes in therapy with decreased likelihood of causing

PT undesirable immune responses.

PT

XX Disclosure; Fig 4c; 57pp; English.

PS

XX In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.

CC The inventor's propose eliminating these allotypes by amino acid changes

CC to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype

CC sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes"

CC should be suitable for therapeutic use in all patients. See AAR27678-

CC R27681. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 110 AA;

Query Match 90.2%; Score 523; DB 2; Length 110;

Best Local Similarity 90.6%; Pred. No. 1.6e-45;

Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 64

Qy 64 QFNSTFRVSVLTIVVHODWLNKKEYCKVSKNGKLPSSIEKTIKTK 109

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 65 QYNSTYRWVSVLTVLHODWLNKKEYCKVSKNGKLPAPIEKTISKAK 110

RESULT 9

AAR41684

ID AAR41684 standard; protein; 110 AA.

XX

XX AAR41684;

XX

XX 25-MAR-2003 (revised)

DT 20-OCT-1993 (first entry)

XX

XX Undefined ORF2 encoded by pAH4602.

XX

XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;

XX chain; variable; constant; region; anti-human; transferrin; receptor;

XX antibody; brain; capillary; endothelial cell; conjugate;

XX neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy;

XX Parkinsons disease; Alzheimers disease.

XX

XX Synthetic.

XX

XX WO9310819-A1.

PN

XX 10-JUN-1993.

PD

XX 24-NOV-1992; 92WO-US010206.

PF

XX

PR 26-NOV-1991; 91US-00800458.
 XX (ALKE-) ALKERMES INC.
 XX
 XX Friden PM;
 XX
 XX WPI; 1993-196742/24.
 DR N-PSDB; AAQ43844.
 XX
 XX Antibody conjugates specific for transferrin receptor - used for
 PT diagnosis and treatment of cancer, AIDS and neurological disorders.
 PT
 XX Disclosure; Fig 11K; 151pp; English.
 XX
 XX The sequences given in AAR41582-85 are encoded by the expression vector,
 CC pAH4602. This vector contains open reading frames encoding the heavy
 CC chain variable region (VH) of the antibody 128.1, an ampicillin
 CC resistance gene and a histidine (histidinol) selection marker.
 CC Transcription of the VH gene is from the VH promoter of the murine 27.44
 CC gene. The vector also includes a heavy chain immunoglobulin enhancer and
 CC the human gamma constant region (CH). The VH region of 128.1 was
 CC isolated by polymerase chain reaction and cloned into plasmid pAH4274.
 CC This was achieved by digesting the plasmid and the product with EcoRV and
 CC NheI. The VH gene was inserted in-frame with the human gamma1 CH region
 CC CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an
 CC anti-human transferrin receptor antibody which binds to the transferrin
 CC receptor on brain capillary endothelial cells. This antibody may be used
 CC in a conjugate in which it is linked to a neuro- pharmaceutical or
 CC diagnostic agent. The conjugate may be used to treat or prevent
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 110 AA;

Query Match 90.2%; Score 523; DB 2; Length 110;
 Best Local Similarity 90.6%; Pred. No. 1.6e-45;
 Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63
 Db : |||||
 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 64
 Qy 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTSKTK 109
 Db : |||||
 65 QYNSTFRVSVLTVLHQDMLNGKEYCKVSNKALPAPIETISKAK 110

RESULT 10
 ADH75385
 ID ADH75385 standard; protein; 110 AA.
 XX
 XX ADH75385;
 AC
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Human IgG1 CH2 region.
 DE
 XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
 KW autoimmune disease; human; IgG; immunoglobulin.
 KW
 XX Homo sapiens.
 OS
 XX
 XX US2004002587-A1.
 PN
 XX
 XX 01-JAN-2004.
 PD
 XX
 XX 20-FEB-2003; 2003US-00370749.
 PF
 XX
 XX 20-FEB-2002; 2002US-0358161P.
 PR
 XX (WATK/) WATKINS J D.
 PA (ALLA/) ALLAN B.
 XX

XX
 XX PI
 XX
 XX WPI; 2004-070755/07.
 DR
 XX
 XX New composition comprising a variant of a parent polypeptide having at
 PT least a portion of a Fe region, useful in treating e.g., autoimmune
 PT diseases.
 PT
 XX Claim 20; SEQ ID NO 23; 62pp; English.
 XX
 XX The invention relates to a new composition comprises a variant of a
 CC parent polypeptide having at least a portion of a Fc region. The variant
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
 CC presence of effector cells more effectively than the parent polypeptide
 CC and comprises at least one amino acid modification at position 280 in the
 CC Fc region. The composition is useful in treating diseases e.g.,
 CC autoimmune diseases. The present sequence represents the amino acid
 CC sequence of a human immunoglobulin G, IgG, CH region.
 XX
 XX Sequence 110 AA;
 SQ
 Query Match 90.2%; Score 523; DB 9; Length 110;
 Best Local Similarity 90.6%; Pred. No. 1.6e-45;
 Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63
 Db : |||||
 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 64
 Qy 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTSKTK 109
 Db : |||||
 65 QYNSTFRVSVLTVLHQDMLNGKEYCKVSNKALPAPIETISKAK 110

RESULT 11
 ADJ52132
 ID ADJ52132 standard; protein; 102 AA.
 XX
 XX ADJ52132;
 AC
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX
 XX CH1 deleted mimetibody-related CH2 peptide SeqID1124.
 DE
 XX
 XX CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW anti-allergic; muscular-Gen; cytostatic; anti-inflammatory; neuroleptic;
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstetric disorder; haematologic disorder; immunologic disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX
 XX Unidentified.
 OS
 XX
 XX WO2004002424-A2.
 PN
 XX
 XX 08-JAN-2004.
 PD
 XX
 XX 30-JUN-2003; 2003WO-US020495.
 PF
 XX
 XX 28-JUN-2002; 2002US-0392431P.
 PR
 XX 19-SEP-2002; 2002US-0412144P.
 PR
 XX (CENZ) CENTOCOR INC.
 PA
 XX

PI Heavner GA, Knight DM, Chrayeb J, Scallion BJ, Neaspor TC;
 XX Kutoloski KA;
 XX WPI; 2004-082872/08.
 XX New CH1 deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic, and
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic, and
 PT nutritional disorders.
 XX
 XX Claim 7; SEQ ID NO 1124; 123pp; English.
 XX
 CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CH1 deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a CH2 peptide which may be used during the creation
 CC of a mimetibody peptide of the invention.
 XX
 XX Sequence 102 AA;
 SQ
 Query Match 90.0%; Score 522; DB 8; Length 102;
 Best Local Similarity 96.1%; Pred. No. 1.9e-45;
 Matches 98; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 8 SVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTKPREQFNS 67
 DB 1 SVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTKPREQFNS 60
 QY 68 TFRVSVSLTVHVDLNGKYEKCKVSNKGLPSSIEKTIKTK 109
 DB 61 TYRVSLSLTVHVDLNGKYEKCKVSNKGLPSSIEKTIKTK 102
 RESULT 12
 AAY42626
 ID AAY42626 standard; protein; 105 AA.
 XX
 AC AAY42626;
 XX
 DT 10-JAN-2000 (first entry)
 XX
 DE Human IgG1 Fc gamma2 residues.
 XX
 KW Immunoglobulin E; IgE; antagonist; Fc epsilon RI receptor; human; bds;
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;
 KW allergic disease.
 XX
 OS Homo sapiens.
 XX
 XX US5965709-A.
 XX
 XX 12-OCT-1999.
 XX
 XX 21-APR-1994; 94US-00232539.
 XX
 XX 14-AUG-1991; 91US-00744768.
 XX
 XX 07-JAN-1994; 94US-00178583.
 XX
 XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;
 XX WPI; 1999-579941/49.
 XX
 PT Immunoglobulin E variants as peptide antagonists useful for raising and
 PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
 PT purification of Fc epsilon RI receptor and in the treatment of allergic
 PT diseases.
 XX
 XX Claim 7; Col 63-64; 37pp; English.
 XX
 CC The invention provides immunoglobulin E (IgE) antagonists comprising one
 CC or more of the Fc epsilon RI receptor-binding determinant sites of human
 CC IgE. The antagonists include IgE variants comprising an immunoglobulin
 CC template and binding determinant sequences (bds) CDBds, EPBds and the
 CC sequence shown in AAY42581. The CDBds (CD loop binding determinant
 CC sequence) are selected from the sequences shown in AAY42567-Y42577 and
 CC the EPBds (EF loop binding determinant sequence) are selected from
 CC sequences shown in AAY42578-Y42580. The variants are useful in raising
 CC and screening anti-IgE antibodies, in the isolation and purification of
 CC Fc epsilon RI receptor and in the treatment and prophylaxis of allergic
 CC diseases
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 90.0%; Score 522; DB 2; Length 105;
 Best Local Similarity 92.3%; Pred. No. 1.9e-45;
 Matches 96; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 6 GPSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTKPREQF 65
 DB 1 GPSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTKPREQF 60
 QY 66 NSTFRVSVSLTVHVDLNGKYEKCKVSNKGLPSSIEKTIKTK 109
 DB 61 NSTFRVSVSLTVHVDLNGKYEKCKVSNKGLPSSIEKTIKTK 104
 RESULT 13
 AAE28089
 ID AAE28089 standard; protein; 109 AA.
 XX
 AC AAE28089;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.
 XX
 KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
 KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
 KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
 KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
 KW virucide.
 XX
 OS Homo sapiens.
 XX
 XX WO200260919-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 12-DEC-2001; 2001WO-US048432.
 XX
 XX 12-DEC-2000; 2000US-0254884P.
 XX
 XX 09-MAY-2001; 2001US-0289760P.
 XX
 XX (MEDI-) MEDIMUNE INC.
 XX
 XX Dall'acqua W, Johnson LS, Ward ES;
 XX WPI; 2002-666925/71.
 XX
 XX Modified immunoglobulins useful in the treatment of autoimmune diseases,
 PT

PT comprises at least one amino acid modification relative to a wild-type
 XX immunoglobulin constant domain.
 PS Disclosure; Page 138; 147pp; English.
 CC The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an IGG constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 CC vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinemia, hypogammaglobulinemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain
 XX
 SQ Sequence 109 AA;
 Query Match 89.3%; Score 518; DB 5; Length 109;
 Best Local Similarity 91.3%; Pred. No. 5.2e-45;
 Matches 95; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
 Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 64
 QY 64 QFNSTRVSVLTVVHODWLNKGEYKCKVSNKGLPSIEKTIISK 107
 Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 65 QYNSTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 108
 RESULT 14
 ADH75415
 ID ADH75415 standard; protein; 110 AA.
 XX
 AC ADH75415;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE CH2 region K290S variant.
 XX
 KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
 KW autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN US2004002587-A1.
 XX
 PD 01-JAN-2004.
 XX
 PF 20-FEB-2003; 2003US-00370749.
 XX
 PR 20-FEB-2002; 2002US-0358161P.
 XX
 PA (WATK/) WATKINS J D.
 PA (ALLA/) ALLAN B.
 XX
 PI Watkins JD, Allan B;
 XX
 DR WPI; 2004-070755/07.
 XX
 PT New composition comprising a variant of a parent polypeptide having at
 PT least a portion of a Fc region, useful in treating e.g., autoimmune
 PT diseases.
 PS Disclosure; SEQ ID NO 53; 62pp; English.
 XX
 CC The invention relates to a new composition comprises a variant of a
 CC parent polypeptide having at least a portion of a Fc region. The variant
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
 CC presence of effector cells more effectively than the parent polypeptide
 CC and comprises at least one amino acid modification at position 280 in the
 CC Fc region. The composition is useful in treating diseases e.g.,
 CC autoimmune diseases. The present sequence represents a CH2 region

CC variant.
 XX Sequence 110 AA;
 SQ
 Query Match 89.3%; Score 518; DB 8; Length 110;
 Best Local Similarity 89.6%; Pred. No. 5.3e-45;
 Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
 Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 64
 QY 64 QFNSTRVSVLTVVHODWLNKGEYKCKVSNKGLPSIEKTIISK 109
 Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 65 QYNSTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 110
 RESULT 15
 ADL90103
 ID ADL90103 standard; protein; 110 AA.
 XX
 AC ADL90103;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human immunoglobulin CH2 region, SEQ ID 2.
 XX
 KW Immune response; immunoglobulin; Ig; CH2 region; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004027049-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 18-SEP-2003; 2003WO-US030188.
 XX
 PR 20-SEP-2002; 2002US-0412219P.
 PR 14-MAR-2003; 2003WO-US007995.
 XX
 PA (ASTR-) ASTRAL INC.
 XX
 PI Bot A, Wang L, Smith D, Phillips B;
 XX
 DR WPI; 2004-295415/27.
 XX
 PT Generating an immune response to an antigen, useful for generating
 PT desired T cell responses comprising administering an immunoglobulin having
 PT one peptide epitope of the antigen attached to the immunoglobulin.
 XX
 PS Disclosure; Page 11; 154pp; English.
 XX
 CC The present invention relates to a method for generating an immune
 CC response to an antigen in a patient. The method comprises administering
 CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
 CC least one peptide epitope of the antigen attached to the Ig or its
 CC portion and administering the immunoglobulin or its portion in
 CC conjunction with a RNA segment. A recombinant human Ig molecule capable
 CC of binding to an Fc gamma receptor (FcgammaR) of an antigen presenting
 CC cell (APC) was used to illustrate the invention. The recombinant human Ig
 CC molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a
 CC hinge region (ADL90104) and a flanking peptide (ADL90105).
 XX
 SQ Sequence 110 AA;
 Query Match 89.1%; Score 517; DB 8; Length 110;
 Best Local Similarity 89.6%; Pred. No. 6.7e-45;
 Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
 Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 64

Qy 64 QFNSTPRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIISKTK 109
Db 65 QYNSTYRWVSVLTVLHQDWLNGKEYCKVFNKALPAPIEKTISKAK 110

Search completed: November 17, 2005, 07:47:00
Job time : 90.0913 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:37:49 ; Search time 16.4247 Seconds
(without alignments)
638.529 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGSFVLPFPKPKOTL.....CKVSNKGLPSSIEKTSKTK 109
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 44790

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277	47.8	88	2 A30503	Ig gamma-2b chain C3 region
2	146	25.2	107	2 168726	IgE chain C3 region
3	146	25.2	107	2 168730	IgE chain C3 region
4	136	23.4	110	2 S43147	Ig epsilon chain C r
5	135	23.3	106	1 K3HU	Ig kappa chain C r
6	131	22.6	99	2 S26653	Ig kappa chain C r
7	130.5	22.5	105	2 B30554	Ig lambda chain C
8	128	22.1	103	2 B26167	Ig lambda chain C
9	124.5	21.5	105	2 B26434	Ig lambda-5 chain
10	120.5	20.8	105	1 L1MS	Ig lambda-1 chain
11	120.5	20.8	105	1 L2HU	Ig lambda chain C
12	120.5	20.8	105	2 S22760	Ig lambda-2 chain
13	119.5	20.6	106	2 S00259	Ig lambda-5 chain
14	118	20.3	102	2 B34509	Ig light chain C r
15	114.5	19.7	98	2 S26854	Ig lambda chain C
16	112.5	19.4	104	2 F53275	Ig kappa-1 chain C
17	111	19.1	99	2 A37927	Ig kappa chain C r
18	109.5	18.9	103	1 K4RB	Ig kappa-B4 chain
19	106.5	18.4	105	2 H32529	Ig lambda chain C
20	104.5	18.0	105	1 L1PG	Ig lambda chain C
21	103	17.8	106	2 I50740	Ig lambda chain C
22	102.5	17.7	109	1 L7RB	Ig lambda chain C
23	102	17.6	106	2 I50741	Ig kappa chain C r
24	100	17.2	104	1 K5RBV	Ig lambda-1 chain
25	100	17.2	105	2 A27390	Ig kappa chain C r
26	100	17.2	106	1 K1MS	Ig kappa chain C r
27	96	16.6	106	1 K4RBS	Ig kappa-2 chain C
28	96	16.6	106	2 G20907	Ig kappa-B4 chain
29	93.5	16.1	102	2 I46731	lambda-chain C-reg

ALIGNMENTS

RESULT 1

A30503
Ig gamma-2b chain C region (E5.7A12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30503
R;Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.
J. Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and constant regions of Ig H chain g
A;Reference number: A30503; MUID:88315788; PMID:2842402
A;Accession: A30503
A;Molecule type: mRNA
A;Residues: 1-88 <GIL>
A;Cross-references: GB:M21925
A;Experimental source: myeloma cell line MPC11
A;Note: the authors translated the codon GAG for residue 41 as Ser
C;Genetics:
A;Introns: 46/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-70/Domain: immunoglobulin homology <IMM>

Query Match 47.8%; Score 277; DB 2; Length 88;
Best Local Similarity 63.2%; Pred. No. 6e-21;
Matches 48; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 23 SRTPEVTCVVVDYSHEDPEVQFNWYDGVGVHNHAKTKPREEQFNSTFRVSVLVVHODW 82
Db 1 SLTPKTCVVVDVSDPDQVQISFWNVNVEVHTAQQTQTHREDYNSTIRVSVSTLPQHQDW 60
Qy 83 LNKGEYKCKVSNKGLP 98
Db 61 MSGKEFKCKVNNKDL 76

RESULT 2

I68726
IgE chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I68726
R;Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s
A;Reference number: I54443; MUID:88152907; PMID:3346043
A;Accession: I68726
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-107 <RES>
A;Cross-references: GB:M22930; NID:G194455; PIDN:AAA37911.1; PID:G194460
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>

Query Match 25.2%; Score 146; DB 2; Length 107;
Best Local Similarity 33.0%; Pred. No. 1.1e-07;
Matches 34; Conservative 19; Mismatches 48; Indels 2; Gaps 2;

Qy	6	GPSVFLPPEPPKQDTLMISRPEVTCVVVDVSHEDPEVFQFNWYVDGVVHNNAKTPRREQF	65
Db	6	GVTYLLPPSPGLD-LYQNGAPKQLCLVVDLSE-KNVNVTWNQSKKTPVSASQWYTKHHH	63
Qy	66	NSTRVVSVLTVVHQDLNGLNKKEYCKCKVSNKGLPSSIETKTSKT	108
Db	64	NATTSTISILPFWAKDMIEGYGCIVDHDPDFPKPIVRSITKT	106

RESULT 3
I68730
IGe chain C3 region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C/Accession: I68730
R/Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A/Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid
A/Reference number: I5443; MUID:88152907; PMID:3346043
A/Accession: I68730
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-107 <RS>
A/Cross-references: GB:M22933; NID:G194464; PIDN:AAA37915.1; PID:G194469
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/22-90/Domain: immunoglobulin homology <IMM>

Query Match	25.2%;	Score 146;	DB 2;	Length 107;
Best Local Similarity	32.3%;	Pred. No. 1.1e-07;		
Matches 37;	Conservative	20;	Mismatches 32;	Indels 26;
Gaps 5;				

Qy	6	GRSFLPFPKPKDTLMISTPEVTCVVUV-SHEDPEVQFN-----WYVDGVEV 53
Db	6	GWITYLIPSPLD-LYQNGAPKLTCLWDLESEKKNVTWNOEKTSVSASQW---TKH 61
Qy	54	HNAKTPREEQFNSTPRVSVLTVVHQDMLNKEYKCKVSNKGLPSSIEKTIISK 108
Db	62	HN-----NATTSITSLPVPAAKWIISGVGYCCIVDHPDFPKPVRSTTKT 106

RESULT 4
S43147
IG upsilon chain - duck (fragment)
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C:Accession: S43147
R:Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
A:Submitted to the EMBL Data Library, March 1994
A:Description: Evidence from duck immunoglobulin genes that IgY is the common ancestor
A:Reference number: S43145
A:Accession: S43147
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <MAG>
A:Cross-references: EMBL:X78355; NID:G468612; PID:G468613
C:Superfamily: immunoglobulin C region; immunoglobulin homology

```

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30554
R;Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:89093962; PMID:2492052
A;Accession: B30554
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-105 <FOL>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-88/Domain: immunoglobulin homology <IMM>

Query Match      22.5%; Score 130.5; DB 2; Length 105;
Best Local Similarity 29.6%; Pred. No. 4e-06;
Matches 32; Conservative 23; Mismatches 46; Indels 7; Gaps 4;

Qy 3 PVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVFQFNWYDVGVH-NAKTKPR 61
Db 2 PKASPSVTLFPFKSEE--LDTNKATVCLLISD--FYPGSVNVVKADGSIINQNKVTQA 57

Qy 62 EEFNSTFRVSVLTIVVHDLWGKEYCKVKSNKGLPSSIEKTSKTK 109
Db 58 SKOSNKIYAASSYLTITGSEWKSSTYCEVTHG--STVTKTVKPSF 103

RESULT 8
B26167
Ig lambda chain C region - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B26167
R;Parvari, R.; Ziv, E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
A;Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a
A;Reference number: A26167; MUID:87218480; PMID:3107981
A;Accession: B26167
A;Molecule type: mRNA
A;Residues: 1-103 <PAR>
A;Cross-references: UNIPROT:P20763; GB:M33049
A;Note: 90-Asp was found in one cDNA clone
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;21-87/Domain: immunoglobulin homology <IMM>

Query Match      22.1%; Score 128; DB 2; Length 103;
Best Local Similarity 29.0%; Pred. No. 7e-06;
Matches 31; Conservative 26; Mismatches 44; Indels 6; Gaps 5;

Qy 3 PVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVFQFNWYDVGVHNAKTKPRE 62
Db 2 PKVAPITLFPSPS-KEELNEATKATLVCLINDF-YPSF-VTVDWVIDG--STRSGETTPAQ 57

Qy 63 EQFNSTFRVSVLTIVVHDLWGKEYCKVKSNKGLPSSIEKTSKTK 109
Db 58 RQNSQVMASSYLSLGSADWSSSHETVTCRVTHNG--TSITKTLKRSE 102

RESULT 9
B26434
Ig lambda-5 chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C;Accession: B26434
R;Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A;Title: Lambda-5, a new light-chain-related locus selectively expressed in pre
A;Reference number: A26434; MUID:87065143; PMID:3024017
A;Accession: B26434
A;Molecule type: mRNA
A;Residues: 1-105 <SAK>

```


Biochemistry 14, 3953-3961, 1975
A;Title: Rotational allomerism and divergent evolution of domains in immunoglobulin light chain C region - western wild mouse
A;Reference number: A90391
A;Contents: annotation; MCG; X-ray crystallography, 2.3 angstroms
R;Hieter, P.A.; Hollis, G.F.; Korsmeyer, S.J.; Waldmann, T.A.; Leder, P.
Nature 294, 536-540, 1981
A;Title: Clustered arrangement of immunoglobulin lambda constant region genes in man.
A;Reference number: A93268; MUID:82086680; PMID:6273747
A;Accession: A93268
A;Molecule type: DNA
A;Residues: 1-105 <HE>
A;Cross-references: GB:J00253; NID:G186118; PIDN:AAA59107.1; PID:G186127
A;Note: six tandem lambda-type genes were identified and the three most 5' were sequenced (lambda-3)
A;Comment: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins Sh, X, and N
C;Genetics:
A;Gene: GDB:IGLC2; IGLC
A;Cross-references: GDB:120691; OMIM:147220
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer
F;20-88/Domain: immunoglobulin homology <IMM>
F;27-86/Disulfide bonds: #status experimental
F;104/Disulfide bonds: interchain (to heavy chain) #status experimental
Query Match 20.8%; Score 120.5; DB 1; Length 105;
Best Local Similarity 27.8%; Pred. No. 4.1e-05;
Matches 30; Conservative 25; Mismatches 46; Indels 7; Gaps 4;
Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61
Db 2 PKAAPSVTLPSPSEEL---LQAKATLVCLISD--FYPCAVTVAWKADSSPVKAGVETTP 57
Qy 62 EEQFNSTFRVSVLTIVVHVDWLNKGYCKVSKNGLPSSIEKTKIS 109
Db 58 SKOSNNKYAASSYLSLTPEQWKSRSYSCQVTHEG--STVEKTVAPTE 103
RESULT 12
S22760
Ig lambda-2 chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
A;Accession: S22760
R;Weiss, S.; Wu, G.E.
EMBO J. 6, 927-932, 1987
A;Title: Somatic point mutations in unrearranged immunoglobulin gene segments encoding the C region of the lambda-2 chain of the mouse (fragment)
A;Reference number: S22759; MUID:87246527; PMID:3109891
A;Accession: S22760
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-106 <WEI>
A;Cross-references: UNIPROT:Q9D8W4; EMBL:X58411; NID:G51763; PIDN:CAA41312.1; PID:G51764
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;21-89/Domain: immunoglobulin homology <IMM>
Query Match 20.8%; Score 120.5; DB 2; Length 106;
Best Local Similarity 29.2%; Pred. No. 4.1e-05;
Matches 31; Conservative 20; Mismatches 48; Indels 7; Gaps 3;
Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61
Db 3 PKSPSVTLPPPSSEEL---ETNKATLVCTITDFYFGVTVVWVKVDGTPVTQGMETTP 58
Qy 62 EEQFNSTFRVSVLTIVVHVDWLNKGYCKVSKNGLPSSIEKTKIS 107
Db 59 SKOSNNKYAASSYLSLTPEQWKSRSYSCQVTHEG--HTVEKSLR 102
RESULT 13

S00259
Ig lambda-5 chain C region - western wild mouse
C;Species: Mus spretus (western wild mouse)
C;Date: 31-Dec-1988 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000
A;Accession: S00259
R;Mami, F.; Cazenave, P.A.; Kindt, T.J.
EMBO J. 7, 117-122, 1988
A;Title: Conservation of the immunoglobulin C-lambda-5 gene in the Mus genus.
A;Reference number: S00259; MUID:88196070; PMID:3129289
A;Accession: S00259
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-106 <MAM>
A;Note: the sequence was translated from the germline gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;21-89/Domain: immunoglobulin homology <IMM>
Query Match 20.6%; Score 119.5; DB 2; Length 106;
Best Local Similarity 29.5%; Pred. No. 5.2e-05;
Matches 31; Conservative 23; Mismatches 44; Indels 7; Gaps 3;
Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61
Db 3 PKSDPLVTLPSPSKNL----QANKTLVCLVSEFPGLVVDWVKVDGVPVTQGVETTP 58
Qy 62 EEQFNSTFRVSVLTIVVHVDWLNKGYCKVSKNGLPSSIEKTKIS 106
Db 59 SKQTNKNKYVSSYLSLTISDQMPHSRYSCRVTHEG--NTVEKSVS 101
RESULT 14
B34509
Ig light chain C region 3 - sandbar shark (fragment)
C;Species: Carcharias plumbeus (sandbar shark)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 17-Nov-2000
A;Accession: B34509
R;Schluter, S.F.; Hohman, V.S.; Edmundson, A.B.; Marchalonis, J.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989
A;Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark
A;Reference number: A34509; MUID:90099382; PMID:2513577
A;Accession: B34509
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-102 <SCH>
A;Cross-references: GB:M29044; NID:G212941; PIDN:AAA49153.1; PID:G212942
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
Query Match 20.3%; Score 118; DB 2; Length 102;
Best Local Similarity 32.6%; Pred. No. 7e-05;
Matches 30; Conservative 17; Mismatches 41; Indels 4; Gaps 3;
Qy 7 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDG-VEVHNAKTKPREQF 65
Db 13 PSVSLPPSP-DOITAKNTATLVCLVSGFKPGAAEIE--WTVDGVRGNGVETSRVQOE 69
Qy 66 NSTFRVSVLTIVVHVDWLNKGYCKVSKNGL 97
Db 70 DNTFVSSYLTLSASDWSHLYSCLVKHEAL 101
RESULT 15
S26654
Ig lambda chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
A;Accession: S26654
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A;Reference number: S26652; MUID:91355693; PMID:2129418
A;Accession: S26654

A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-98 <EHR>
A;Cross-references: EMBL:X65286
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-88/Domain: immunoglobulin homology <IMM>

Query Match	19.7%	Score 114.5;	DB 2;	Length 98;
Best Local Similarity	29.1%	Pred. No. 0.00015;		
Matches	30;	Conservative	21;	Mismatches 45; Indels 7; Gaps 4;

Qy	3	PVAGPSVFLPPPKDLMISRTEVTCVVVDVSHEDPEVQFNWYVDGVEVH-NAKTKPR	61
Db	2	PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYFGAVTVAKADSSPVKAGVETTP	57

Qy	62	BEQFNSTFRVSVLTVVHQDLNGKEYCKKVSNGKGLPSSIEKT	104
Db	58	SKQSNKYYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKT	98

Search completed: November 17, 2005, 07:55:07
Job time : 16.4247 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.1461 Seconds
(without alignments)
723.518 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGPSVFLPPPKPDTL.....CKVSNKGLPSSIBKTSKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	135	23.3	106	1 KAC_HUMAN	P01834 homo sapien
2	128	22.1	103	1 LAC_CHICK	P20763 gallus gall
3	123.5	21.3	106	2 Q8TCJ5	Q8tcj5 homo sapien
4	120.5	20.8	105	1 LAC1_MOUSE	P01843 mus musculus
5	120.5	20.8	105	1 LAC1_HUMAN	P01842 homo sapien
6	119.5	20.6	105	1 LAC5_MUSP	P20765 mus spratus
7	115.5	19.9	105	1 LAC5_MOUSE	P20764 mus musculus
8	109.5	18.9	103	1 KAC4_RABIT	P01840 oryctolagus
9	104.5	18.0	105	1 LAC_FIG	P01846 sus scrofa
10	102.5	17.7	105	1 KAC6_RABIT	P01847 oryctolagus
11	100	17.2	104	1 KAC5_RABIT	P01984 oryctolagus
12	100	17.2	104	1 LAC1_RAT	P20766 rattus norv
13	100	17.2	106	1 KAC_MOUSE	P01837 mus musculus
14	96	16.6	106	1 KACB_MOUSE	P01839 oryctolagus
15	92	15.9	106	1 KACB_RAT	P01835 rattus norv
16	90	15.5	104	1 KAC9_RABIT	P01838 oryctolagus
17	90	15.5	104	1 LAC2_RAT	P20767 rattus norv
18	88	15.2	103	1 KAC5_RABIT	P01841 oryctolagus
19	87	15.0	106	1 KACA_RAT	P01836 rattus norv
20	86	14.8	104	1 LAC3_MOUSE	P01845 mus musculus
21	79	13.6	104	1 LAC2_MOUSE	P01844 mus musculus
22	79	13.6	105	2 Q99JC1	Q99jc1 mus musculus
23	67	11.6	107	2 Q8KY10	Q8ky10 bacillus an
24	67	11.6	107	2 Q6E215	Q6e215 bacillus an
25	65.5	11.3	74	2 P79659	P79659 oncorhynch
26	65.5	11.3	74	2 P79650	P79650 oncorhynch
27	63	10.9	91	2 Q31248	Q31248 peromyscus
28	62.5	10.8	104	2 Q30837	Q30837 ovis aries
29	62	10.7	79	1 SNRP_HUMAN	P80697 homo sapien
30	61	10.5	73	2 Q8FBY4	Q8fby4 escherichia
31	61	10.5	93	2 Q6LBV9	Q6lbv9 mus musculus

RESULT 1
KAC_HUMAN
ID KAC_HUMAN STANDARD; PRT; 106 AA.
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 23-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain C region.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gattlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;
RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steimetz-Kayne M., Suter L., Watanabe S.;
RT (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;

ALIGNMENTS

32	60.5	10.4	74	2	P79661
33	60.5	10.4	93	2	Q6LBW2
34	60	10.3	102	2	Q8HB97
35	59.5	10.3	55	2	Q768W8
36	59.5	10.3	92	2	O41412
37	59	10.2	91	2	Q9JKP1
38	59	10.2	98	2	Q7XZF9
39	59	10.2	99	2	Q9DG61
40	59	10.2	100	2	Q649X2
41	59	10.2	106	2	Q31261
42	58.5	10.1	74	2	P79652
43	58.5	10.1	74	2	P79657
44	58.5	10.1	93	2	O19471
45	58.5	10.1	93	2	O19472

P79661 oncorhynchu
Q6lbw2 mus musculu
Q8hb97 podarcis hi
Q768w8 uncultured
O41412 human immun
Q9jkl1 marmota mon
Q9kzf9 oryza sativ
Q9dg61 salmo salar
Q649x2 uncultured
Q31261 rattus norv
P79652 oncorhynchu
P79657 oncorhynchu
O19471 mus musculu
O19472 mus musculu

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
 type).",
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [7]
 RP SEQUENCE (BENCE-JONES PROTEIN AG).
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RL complete sequence and the location of the disulfide bridges.";
 RJ J. Biol. Chem. 244:3550-3560(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 RL chains.";
 RJ Science 169:56-59(1970).
 RN [9]
 RP SEQUENCE OF 1-33; 38-41 AND 62-80.
 RC TISSUE=Abdominal adipose tissue;
 RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
 RA Olsen K.E., Sletten K., Westermarck P.;
 RT "Extended analysis of AL-amyloid protein from abdominal wall
 RL subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
 RJ Biochem. Biophys. Res. Commun. 245:713-716(1998).
 CC -!- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker,
 CC Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic
 CC marker, Ala-45 and Leu-83.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 CC EMBL; J00241; AAA58989.1; -.
 DR PIR; B90562; K3HU.
 DR PDB; 1D5B; X-ray; A/L=1-103.
 DR PDB; 1D51; X-ray; L=1-103.
 DR PDB; 1D6V; X-ray; L=1-103.
 DR PDB; 1HEZ; X-ray; -.
 DR PDB; 1HKL; X-ray; L=1-106.
 DR PDB; 1I72; X-ray; A/C=1-106.
 DR PDB; 1MIM; X-ray; L=1-105.
 DR Genew; HGNC:5716; IGKC.
 DR H-invDB; HIX0021121; -.
 DR MIM; 147200; -.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR 3D-structure; Direct protein sequencing; Immunoglobulin C region;
 DR Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN 5 102 Ig-like.
 FT DISULFID 26 86
 FT DISULFID 106 106 Interchain (with a heavy chain).
 FT VARIANT 83 83 V -> L (in INV(1,2) marker).
 FT CONFLICT 14 14 /FTId=VAR_003897.
 FT CONFLICT 57 57 D -> N (in Ref. 7 and 8).
 FT STRAND 3 3 E -> Q (in Ref. 5 and 6).
 FT STRAND 6 10
 FT HELIX 14 17
 FT TURN 18 20
 FT STRAND 21 32
 FT STRAND 37 42

FT TURN 43 44
 FT STRAND 45 47
 FT STRAND 51 55
 FT TURN 60 62
 FT STRAND 65 74
 FT HELIX 75 79
 FT TURN 80 80
 FT STRAND 83 89
 FT TURN 91 92
 FT TURN 97 102
 FT TURN 103 104
 SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
 Query Match 23.1%; Score 135; DB 1; Length 106;
 Best Local Similarity 31.1%; Pred. No. 9.5e-06;
 Matches 33; Conservative 26; Mismatches 41; Indels 6; Gaps 3;
 QY 4 VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDG--EVHNAKTKPR 61
 DB 2 VAAPSVFIPP--PSDQLKSGTASVVCLLNNFYPREAKVQ--WKVDNALQSGNSQESVTE 57
 QY 62 EEQFNSTFRVSVLTVVHQLNGKEYKCKVSNKGLPSSIEKTISK 107
 DB 58 QDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNR 103
 RESULT 2
 LAC_CHICK
 ID - LAC_CHICK STANDARD; PRT; 103 AA.
 AC P20763;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain C region.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87218480; PubMed=3107981;
 RA Parvavi R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
 RT "Analyses of chicken immunoglobulin light chain cDNA clones indicate a
 RL few germline V lambda genes and allotypes of the C lambda locus.";
 RL EMBO J. 6:97-102(1987).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 CC EMBL; X04768; CAA28461.1; -.
 DR FIR; B26167; B26167.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin C region; Immunoglobulin domain; Polymorphism.
 FT NON_TER 1 1
 FT DOMAIN 6 99 Ig-like.
 FT DISULFID 28 85
 FT DISULFID 103 103 Interchain (with heavy chain).
 FT VARIANT 90 90 N -> D.
 SQ SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;


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Query Match      22.1%; Score 128; DB 1; Length 103;
Best Local Similarity 29.0%; Pred. NO. 4.6e-05;
Matches 31; Conservative 26; Mismatches 44; Indels 6; Gaps 5;

QY 3 PVAGPSVLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPR 62
DB 2 PKVAPITLFPSPS-KEELNEATKATLVCLINDF-YPSP-VTVDWVIDG-STRSGETTPAQ 57
QY 63 EQFNSTFRVSVLTVVHVDWLNKGYKCKVSNKGLPSSIEKTIKTK 109
DB 58 RQSNQYMASSVLSLSASDSSSHETTCRVTHNG--TSITKTLKRE 102

RESULT 3
ID Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp667J0810 (Fragment).
GN Name=DKFZp667J0810;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -
DR HSP; P01842; ILLI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 106 AA; 11265 MW; 1452728B65F4565 CRC64;

Query Match      21.3%; Score 123.5; DB 2; Length 106;
Best Local Similarity 28.7%; Pred. NO. 0.00013;
Matches 31; Conservative 24; Mismatches 46; Indels 7; Gaps 4;

QY 3 PVAGPSVLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61
DB 3 PKAAPSVTLFPSSSE--LQANKATLVCLISD--FYQAVTVANKASSPKAGVETTP 58
QY 62 EQFNSTFRVSVLTVVHVDWLNKGYKCKVSNKGLPSSIEKTIKTK 109
DB 59 SKQSNKYAASSVLSLTPEQMKSHKSYSCQVTHEG--STVEKTVAPTE 104

RESULT 4
LAC1 MOUSE
ID LAC1 MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Seising E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=81148806; PubMed=6259534;
RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Gefter M.L., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL Nature 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=8220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC -!- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
CC normal lambda-2 chain and 1 abnormal lambda-1 chain that is
CC missing a large part of the V region. The C region sequence (shown
CC here) appears completely normal.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; J00582; AAA51636.1; -.
CC EMBL; J00587; AAB59672.1; -.
CC PIR; A93922; LIMS.
CC PDB; 1JNH; X-ray; A=1-105.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
FT NON TER 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86 Interchain (with heavy chain).
FT DISULFID 104 104 ET -> TE (in Ref. 4).
FT CONFLICT 19 20 Q -> E (in Ref. 4).
FT CONFLICT 56 56 Missing (in Ref. 4).
FT CONFLICT 75 75 HS -> SH (in Ref. 4).
FT CONFLICT 81 82 S -> SS (in Ref. 4).
FT CONFLICT 85 85 E -> Q (in Ref. 4).
FT CONFLICT 96 96
FT STRAND 4 4
FT STRAND 7 7
FT STRAND 10 11
FT STRAND 15 19
FT HELIX 20 21
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 52 54
FT STRAND 58 60
FT TURN 61 63
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FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; 11575 MW; A99F2B09BCFCA018 CRC64;

Query Match 20.8%; Score 120.5; DB 1; Length 105;
Best Local Similarity 29.2%; Pred. No. 0.00027;
Matches 31; Conservative 20; Mismatches 48; Indels 7; Gaps 3;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNYYVDGVEY-HNAKTKPR 61
DB 2 PKSPSVTLFPSPSEEL-----ETNKATLVCTITDFYFGVVTVDWKVDGTPVTQGMETTP 57

QY 62 EEQFNSTFRVSVLTVVHQDLNCKEYKCKVSNKGLPSSLEKTIISK 107
DB 58 SKQSNKYMSSYLTLTARAWERHSSYSCQVTHEG--HTVEKLSLR 101

RESULT 5
LAC_HUMAN STANDARD; PRT; 105 AA.
AC P01842; F80423;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG lambda chain C regions.
GN Name=IGLC1;
GN and
GN Name=IGLC2;
GN and
GN Name=IGLC3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN SH).
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176 (1970).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX MEDLINE=69088380; PubMed=4883841;
RA Milstein C., Clegg J.B., Jarvis J.M.;
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT Bence-Jones protein."
RL Biochem. J. 110:631-652 (1968).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN NTG-64).
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup."
RL J. Biochem. 93:421-429 (1983).
RN [4]
RP SEQUENCE (BENCE-JONES PROTEIN KERN).
RX MEDLINE=71150336; PubMed=5549568;
RA Ponstingl H., Hess M., Hilschmann N.;
RT "Structural rule of antibodies. Primary structure of a monoclonal
RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT protein Kern). V. The complete amino acid sequence and its genetic
RT interpretation."
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266 (1971).
RN [5]
RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX MEDLINE=74109253; PubMed=4814721;
RA Chen B.L., Poljak R.J.;

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RT "Amino acid sequence of the (lambda) light chain of a human myeloma
RT immunoglobulin (IG New)."
RL Biochemistry 13:1295-1302 (1974).
RN [6]
RP SEQUENCE (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins."
RL Eur. J. Biochem. 228:886-893 (1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX MEDLINE=75046825; PubMed=4215080;
RA Poljak R.J., Anzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA Saul F.;
RT "The three-dimensional structure of the fab' fragment of a human
RT myeloma immunoglobulin at 2.0-A resolution."
RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444 (1974).
RN [8]
RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX MEDLINE=75013804; PubMed=4415202;
RA Felt J.W., Deutsch H.F.;
RT "Primary structure of the Mcg lambda chain."
RL Biochemistry 13:4102-4114 (1974).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RX Edmondson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
RT immunoglobulin light chains."
RL Biochemistry 14:3953-3961 (1975).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmondson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms."
RL J. Mol. Biol. 210:601-615 (1989).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=82080680; PubMed=6273747;
RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT "Clustered arrangement of immunoglobulin lambda constant region genes
RT in man."
RL Nature 294:536-540 (1981).
CC -!- MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain
CC found in proteins SH, X, and NIG-84. The Kern protein has the
CC Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein
CC has the Kern+ marker, and the Mcg+ marker.
CC -!- MISCELLANEOUS: Six tandem lambda-type genes were identified and
CC the 3 most 5' were sequenced. These correspond to the Mcg sequence
CC (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+
CC sequence (lambda-3).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; J00253; AAA59107.1; -
CC EMBL; L38582; AAB36581.1; ALT_INIT.
CC EMBL; X51754; CAB38569.1; ALT_INIT.
CC EMBL; X51755; CAA36049.1; -
CC EMBL; X51755; CAA36051.1; -
CC PIR; A92057; L2HU.
CC PDB; 1AOK; X-ray; L=1-105.
CC PDB; 1LIL; X-ray; A/B=1-105.
CC PDB; 2MCG; X-ray; -
CC PDB; 7FAB; X-ray; L=1-105.

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DR Genew; HGNC:5855; IGLC1.
DR Genew; HGNC:5856; IGLC2.
DR Genew; HGNC:5857; IGLC3.
DR H-InvDB; HIX0016285; -.
DR MIM; 147220; -.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR PROSITE; PS00290; IG_MHC.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
FT VARIANT 5 5
FT VARIANT 7 7
FT VARIANT 45 45
FT VARIANT 56 56
FT VARIANT 82 82
FT STRAND 8 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 24 32
FT STRAND 38 43
FT TURN 44 45
FT STRAND 46 48
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 72
FT HELIX 75 80
FT STRAND 84 89
FT STRAND 94 99
SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match 20.8%; Score 120.5; DB 1; Length 105;
Best Local Similarity 27.8%; Pred. No. 0.00027;
Matches 30; Conservative 25; Mismatches 46; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPKPKOTLMTISRTEVTCVVVDVSHEDPEVFQWYVDGVEVH-NAKTKPR 61
DB 2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYFGAVTVAKADSSPVKAGVETTP 57

QY 62 EEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109
DB 58 SKQSNKYAASSYLSLTPQMKSHRSYSCQWTHG--STVEKTVAPTE 103

RESULT 6
LACS MUSSP
ID LACS_MUSSP STANDARD; PRT; 105 AA.
AC P20765;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-5 chain C region.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88196070; PubMed=3129289;
RA Mani F.; Cazenave P.A.; Kindt T.J.;
RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";

EMBO J. 7:117-122(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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EMBL; M35582; AAA39152.1; -.
HSSP; P01843; LUNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11674 MW; AAB417DF68471A17 CRC64;

Query Match 20.6%; Score 119.5; DB 1; Length 105;
Best Local Similarity 29.5%; Pred. No. 0.00033;
Matches 31; Conservative 23; Mismatches 44; Indels 7; Gaps 3;

QY 3 PVAGPSVFLPPKPKOTLMTISRTEVTCVVVDVSHEDPEVFQWYVDGVEVH-NAKTKPR 61
DB 2 PKSDPLVTLFPLSKNL---QANKVTLVCLVSEFYPTGLVVDWKVDGVPVTCQGVETTP 57

QY 62 EEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTIK 106
DB 58 SKQTNKMYVSVSYLTLSIDQMPHRSYSCRVTHEG--NTVEKSVS 100

RESULT 7
LACS MOUSE
ID LACS_MOUSE STANDARD; PRT; 105 AA.
AC P20764;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-5 chain C region.
GN Name=Igl-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065143; PubMed=3024017;
RA Sakaguchi N.; Melchers F.;
RT "Lambda 5, a new light-chain-related locus selectively expressed in
pre-B lymphocytes.";
RL Nature 324:579-582(1986).
CC -!- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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EMBL; M30387; -. NOT_ANNOTATED_CDS.
HSSP; P01843; LUNH.

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DR MGD; MGI:96529; Igl-5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON TER 1 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11678 MW; 1F210915904A86A5 CRC64;

Query Match 19.9%; Score 115.5; DB 1; Length 105;
Best Local Similarity 30.5%; Pred. No. 0.00084;
Matches 32; Conservative 25; Mismatches 41; Indels 7; Gaps 5;

QY 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEV-HNAKTKPR 61
Db 2 PKSDPLVTLFPLSKN-LQPTR-PQLVCLVSE--FYPGTLVDWKVDGVPVPTQGVETTPQ 57
QY 62 EQENSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIIS 106
Db 58 SKOTNNKYMVSSYLTLLISDQMPHSRTSCRVTHEG--NTVEKSVS 100

RESULT 8
KAC4_RABIT
ID_KAC4_RABIT STANDARD; PRT; 103 AA.
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6411231;
RA Emorine L.; Dreher K.B.; Kindt T.J.; Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT allotype J-C locus and evidence for several b4-related sequences in
RT the rabbit genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O.; Auffray C.; Cazenave P.-A.; Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S.; Kindt T.J.; Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
RT to streptococcal carbohydrate. II. Sequence determination of peptides
RT from tryptic and peptic digests.";
RL J. Biol. Chem. 250:3289-3296(1975).
CC -1- MISCELLANEOUS: This chain was obtained from antibody to the
CC specific carbohydrate of group C Streptococci and was isolated
CC from the serum of a single rabbit.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC -----
DR EMBL; X00231; CAA25051.1; -.
DR PIR; A93971; K4RB.
DR HSSP; P01837; ILCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1 95 Ig-like.
FT DOMAIN 5 95
FT DISULFID 26 85 Interchain (with a heavy chain).
FT DISULFID 103 103 N -> D (in Ref. 3).
FT CONFLICT 58 58
SQ SEQUENCE 103 AA; 11043 MW; 5FCSACCB60E68DB CRC64;

Query Match 18.9%; Score 109.5; DB 1; Length 103;
Best Local Similarity 30.8%; Pred. No. 0.0033;
Matches 32; Conservative 20; Mismatches 39; Indels 13; Gaps 6;

QY 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVE---VHNAKT 58
Db 2 PVA-PTVLIFPPAADO--VATGTVITVCV---ANKYFPDVTVTWEVDGTTQTGTIENSKT 55
QY 59 KPREEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIE 102
Db 56 P--QNSADCTYNLSLTLTSTQYNSHKYCTCKVT-QGTTSVVQ 96

RESULT 9
LAC_PIG
ID_LAC_PIG STANDARD; PRT; 105 AA.
AC P01846;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78000254; PubMed=409425;
RA Novotny J.; Franek F.; Margolies M.N.; Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
RT immunoglobulin lambda chains.";
RL Biochemistry 16:3765-3772(1977).
CC -1- MISCELLANEOUS: This chain was obtained from a mixture of normal
CC immunoglobulins.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02129; L1PG.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1 100 Ig-like.
FT DOMAIN 2 100
FT DISULFID 27 86 Interchain (with heavy chain).
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match 18.0%; Score 104.5; DB 1; Length 105;
Best Local Similarity 27.5%; Pred. No. 0.011;
```



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FT STRAND 3 3
FT STRAND 6 10
FT HELIX 14 17
FT TURN 18 20
FT STRAND 21 32
FT STRAND 37 42
FT STRAND 43 44
FT TURN 45 47
FT STRAND 49 50
FT TURN 51 55
FT STRAND 60 62
FT STRAND 65 74
FT HELIX 75 79
FT TURN 80 80
FT STRAND 83 89
FT TURN 91 92
FT STRAND 97 102
FT TURN 103 106
SQ SEQUENCE 106 AA; 11778 MW; 4B51PF5EF49BAE85 CRC64;

Query Match 17.2%; Score 100; DB 1; Length 106;
Best Local Similarity 24.3%; Pred. No. 0.03;
Matches 26; Conservative 25; Mismatches 50; Indels 6; Gaps 3;

Qy 5 AGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQWYVDGVEVHNA--KTKPRE 62
Db 3 AAPTSTVSPSSSEQ--LTSGGASVVCFLNNFPKQ--INVKKIDGSRQNGVLNWTQ 58

Qy 63 EQFNSTRFRVSVLTVDHQLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 59 DSKDSTVMSSTLTVDKDEYHRHSYTCETHKTSPTPIVKSFRNRE 105

RESULT 14
KACB RABIT
ID KACB RABIT STANDARD; PRT; 106 AA.
AC P01833;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa-b4 chain C region.
GN Name=K-BAS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Basilea;
RX PubMed=11894960;
RA Heidmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit
RL genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
RL EMBL J. 2:437-441(1983).
CC -1- MISCELLANEOUS: In Basilea rabbits, the major type of light chain
CC is lambda. The kappa chain shown is a minor component. All other
CC rabbit B allotypes have Cys-64.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; V01241; CAA24558.1; -
CC EMBL; V00885; -; NOT_ANNOTATED_CDS.
DR PIR; A02121; K4RBB5.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

```

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DR Pfam; PF00047; ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 87
FT DISULFID 106 106 Interchain (with a heavy chain).
SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 16.6%; Score 96; DB 1; Length 106;
Best Local Similarity 28.4%; Pred. No. 0.076;
Matches 31; Conservative 22; Mismatches 44; Indels 12; Gaps 6;

Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQWYVDGVE---VHNAKT 58
Db 3 PVA-PSVLLFPSPKEE--LTGTATIVCVANKFPSPD--ITVTWKVDGTTQQSGIENSKT 57

Qy 59 KPREEQFNSTRFRVSVLTVDHQLNGKEYKCKVSNKGLPSSIEKTIK 107
Db 58 POSPE--DNTYLSLSLTSLTSAQYNHSHSVTCEVV--QGSASPIVQSFNR 103

RESULT 15
KACB RAT
ID KACB RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Louvain;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong selection
RL at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RL phylogenetic relationships of V- and C-region genes.";
RL J. Immunol. 115:59-62(1975).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93301; KIRTB.
DR HSSP; P01837; IORS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1
FT DOMAIN 5 102 Ig-like.
FT DISULFID 26 86 Interchain (with a heavy chain).
FT DISULFID 106 106 D -> N (in Ref. 2).
FT CONFLICT 2 2 N -> K (in Ref. 2).
FT CONFLICT 30 30 Missing (in Ref. 2).
FT CONFLICT 48 48 E -> Q (in Ref. 2).
FT CONFLICT 79 79 E -> Q (in Ref. 2).
FT CONFLICT 87 87 E -> Q (in Ref. 2).
FT CONFLICT 98 98 V -> VW (in Ref. 2).
FT CONFLICT 100 100 S -> N (in Ref. 2).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.3927 Seconds
(without alignments)
347.833 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGSVFLFPKPKDTL.....CKVSNKGLPSIEKTSKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	98.6	109	3	US-08-444-644-30
2	572	98.6	109	3	US-08-232-246A-30
3	536	92.4	109	2	US-08-070-116A-4
4	536	92.4	109	4	US-08-557-050-4
5	536	92.4	110	3	US-08-444-644-44
6	536	92.4	110	3	US-08-232-246A-44
7	523	90.2	110	3	US-08-444-644-21
8	523	90.2	110	3	US-08-232-246A-21
9	522	90.0	105	2	US-08-232-539D-60
10	514	88.6	110	3	US-08-444-644-38
11	514	88.6	110	3	US-08-232-246A-38
12	321	55.3	66	3	US-08-569-147-85
13	175	30.2	107	4	US-09-281-760E-36
14	172.5	29.7	106	2	US-08-232-539D-54
15	158	27.2	109	3	US-08-466-163B-1
16	158	27.2	109	4	US-09-802-096-1
17	158	27.2	109	4	US-09-802-077-1
18	138	23.8	100	1	US-08-422-101-10
19	138	23.8	100	1	US-08-422-091-10
20	138	23.8	100	2	US-08-422-092-10
21	138	23.8	100	2	US-08-788-800-7
22	138	23.8	100	3	US-08-422-093-10
23	138	23.8	100	3	US-08-422-112-10
24	135	23.3	105	3	US-09-025-769B-166
25	135	23.3	105	4	US-09-490-070A-166
26	135	23.3	105	4	US-09-490-153-166
27	135	23.3	105	4	US-09-490-324-166

28	135	23.3	106	2	US-08-378-939-40	Sequence 40, Appl
29	135	23.3	106	2	US-08-761-277A-49	Sequence 49, Appl
30	135	23.3	106	3	US-08-444-644-26	Sequence 26, Appl
31	135	23.3	106	3	US-08-232-246A-26	Sequence 26, Appl
32	135	23.3	107	1	US-08-422-101-8	Sequence 8, Appl
33	135	23.3	107	1	US-08-422-091-8	Sequence 8, Appl
34	135	23.3	107	2	US-08-422-092-8	Sequence 8, Appl
35	135	23.3	107	2	US-08-788-800-5	Sequence 5, Appl
36	135	23.3	107	3	US-08-422-093-8	Sequence 8, Appl
37	135	23.3	107	3	US-08-422-112-8	Sequence 8, Appl
38	135	23.3	107	4	US-09-301-593-20	Sequence 20, Appl
39	135	23.3	108	4	US-09-313-942-13	Sequence 13, Appl
40	131	22.6	106	1	US-08-399-106A-7	Sequence 7, Appl
41	131	22.6	106	1	US-08-433-105A-7	Sequence 7, Appl
42	131	22.6	106	2	US-08-434-869A-7	Sequence 7, Appl
43	126	21.7	106	2	US-08-378-939-42	Sequence 42, Appl
44	124.5	21.5	109	2	US-08-646-981-6	Sequence 6, Appl
45	124	21.4	109	1	US-08-436-463-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-30

Query Match      98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 1 APPVAGSVLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPSSIEKTIKTK 109
DB 61 REEQFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTIKTK 109

RESULT 3
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-116A-4

Query Match      92.4%; Score 536; DB 2; Length 109;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVLFPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63
DB 4 LGPSVLFPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63
QY 64 QFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPSSIEKTIKTK 109
DB 64 QFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 4
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF

```

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; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match 92.4%; Score 536; DB 4; Length 109;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

Qy 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 5
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 601555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match 92.4%; Score 536; DB 4; Length 109;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

Qy 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 6
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-44

Query Match 92.4%; Score 536; DB 3; Length 110;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 64

Qy 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 110

RESULT 6
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-44

Query Match 92.4%; Score 536; DB 3; Length 110;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
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5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 64

QY 64 QFNSTRVSVVLTVHVDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 QFNSTRVSVVLTVHVDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 110

RESULT 7
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-21

Query Match 90.2%; Score 523; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 9.5e-54;
Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 64

QY 64 QFNSTRVSVVLTVHVDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 QFNSTRVSVVLTVHVDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 110

RESULT 8
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240

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; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-232-246A-21

Query Match 90.2%; Score 523; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 9.5e-54;
Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 64

QY 64 QFNSTRVRSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 65 QYNSTRVRSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110

RESULT 9
US-08-232-539D-60
; Sequence 60, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: 19e Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/74768
; FILING DATE: 14-AUG-1991
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-232-539D-60

Query Match 90.0%; Score 522; DB 2; Length 105;
Best Local Similarity 92.3%; Pred. No. 1.2e-53;
Matches 96; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREEQF 65

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-232-246A-21

Query Match 90.2%; Score 523; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 9.5e-54;
Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 64

QY 64 QFNSTRVRSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 65 QYNSTRVRSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110

RESULT 10
US-08-444-644-38
; Sequence 38, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-444-644-38

Query Match 88.6%; Score 514; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 1.1e-52;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
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QY 64 QFNSTRVRSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 65 QYNSTRVRSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110
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RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION DATA: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match      88.6%; Score 514; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 1.1e-52;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
Db      5 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKLREE 64

QY      64 QFNSTFRVSVLTFLVHQDWLNGKEYKCKVSNKGLPSSIEKTTISKTK 109
Db      65 QYNSTFRVSVLTFLVHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
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; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match      55.3%; Score 321; DB 3; Length 66;
Best Local Similarity 93.5%; Pred. No. 2.5e-30;
Matches 58; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
Db      5 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 64

QY      64 QF 65
Db      65 QY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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Db 65 NGTLVTSTLPVGTDRWIEG-ETQCRVTHPHLPALMRSTTKT 106

Search completed: November 17, 2005, 07:53:55
Job time : 23.3927 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 82.3721 Seconds
(without alignments)
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Title: US-09-674-857-2

Perfect score: 580

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Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	572	98.6	109 18	US-10-959-318-2
2	564	97.2	109 18	US-10-959-318-17
3	564	97.2	109 18	US-10-959-318-18
4	554	95.5	109 18	US-10-959-318-11
5	554	95.5	109 18	US-10-959-318-12
6	543.5	93.7	110 18	US-10-959-318-9
7	543.5	93.7	110 18	US-10-959-318-10
8	540	93.1	109 18	US-10-959-318-15
9	540	93.1	109 18	US-10-959-318-16
10	538.5	92.8	110 20	US-11-018-102-25
11	536	92.4	109 14	US-10-267-286A-4

12	536	92.4	110	18	US-10-959-318-4	Sequence 4, Appli
13	536	92.4	110	18	US-10-959-318-21	Sequence 21, Appl
14	536	92.4	110	20	US-11-018-102-24	Sequence 24, Appl
15	529.5	91.3	110	18	US-10-959-318-13	Sequence 13, Appl
16	529.5	91.3	110	18	US-10-959-318-14	Sequence 14, Appl
17	529	91.2	110	18	US-10-959-318-3	Sequence 3, Appli
18	529	91.2	110	18	US-10-959-318-7	Sequence 7, Appli
19	529	91.2	110	18	US-10-959-318-8	Sequence 8, Appli
20	528	91.0	109	18	US-10-627-556-270	Sequence 270, App
21	525.5	90.6	110	20	US-11-018-102-23	Sequence 23, Appl
22	523	90.2	109	14	US-10-207-655-220	Sequence 220, App
23	523	90.2	109	18	US-10-627-556-14	Sequence 14, Appl
24	523	90.2	110	15	US-10-370-749-23	Sequence 23, Appl
25	523	90.2	110	18	US-10-959-318-1	Sequence 1, Appli
26	523	90.2	110	20	US-11-018-102-22	Sequence 22, Appl
27	522	90.0	102	18	US-10-609-783B-57	Sequence 57, Appl
28	522	90.0	102	18	US-10-609-783B-59	Sequence 59, Appl
29	522	90.0	109	18	US-10-627-556-302	Sequence 302, App
30	521	89.8	110	18	US-10-959-318-19	Sequence 19, Appl
31	521	89.8	110	18	US-10-959-318-20	Sequence 20, Appl
32	519	89.5	109	18	US-10-627-556-294	Sequence 294, App
33	518	89.3	109	14	US-10-020-354-80	Sequence 80, Appl
34	518	89.3	109	18	US-10-627-556-258	Sequence 258, App
35	518	89.3	109	18	US-10-627-556-278	Sequence 278, App
36	518	89.3	110	15	US-10-370-749-53	Sequence 53, Appl
37	516	89.0	110	15	US-10-370-749-51	Sequence 51, Appl
38	516	89.0	110	18	US-10-959-318-22	Sequence 22, Appl
39	515	88.8	109	14	US-10-207-655-322	Sequence 322, App
40	515	88.8	109	18	US-10-627-556-92	Sequence 92, Appl
41	515	88.8	110	18	US-10-959-318-5	Sequence 5, Appli
42	515	88.8	110	18	US-10-959-318-6	Sequence 6, Appli
43	515	88.8	110	18	US-10-959-318-25	Sequence 25, Appl
44	514	88.6	110	18	US-10-959-318-23	Sequence 23, Appl
45	514	88.6	110	18	US-10-959-318-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-2

Query Match 98.6%; Score 572; DB 18; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.6e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	APPVAGPSVFLFPKPKDTLMI	SRTPVTCVVVDVSHEDDEVGFN	WYVDGVEVHNATKP	60
Db	1	APPVAGPSVFLFPKPKDTLMI	SRTPVTCVVVDVSHEDDEVGFN	WYVDGVEVHNATKP	60
Qy	61	REEQFNSTFRVSVLT	VVHODWLNKGEYKCKVSNKGLP	SSIEKTIKTK	109
Db	61	REEQFNSTFRVSVLT	VVHODWLNKGEYKCKVSNKGLP	SSIEKTIKTK	109

```
RESULT 2
US-10-959-318-17
; Sequence 17, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta d (D268) mutation
US-10-959-318-17

Query Match          97.2%; Score 564; DB 18; Length 109;
Best Local Similarity 97.2%; Pred. No. 9.6e-48;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

Qy 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIETIKTK 109

RESULT 3
US-10-959-318-18
; Sequence 18, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta e (E268) mutation
US-10-959-318-18

Query Match          97.2%; Score 564; DB 18; Length 109;
Best Local Similarity 97.2%; Pred. No. 9.6e-48;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVSEDPVFQFNWYVDGVEVHNAKTKP 60
```

```
Qy 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIETIKTK 109

RESULT 4
US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
US-10-959-318-11

Query Match          95.5%; Score 554; DB 18; Length 109;
Best Local Similarity 94.5%; Pred. No. 9.2e-47;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

Qy 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109

RESULT 5
US-10-959-318-12
; Sequence 12, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and e (E268)
US-10-959-318-12

Query Match          95.5%; Score 554; DB 18; Length 109;
Best Local Similarity 94.5%; Pred. No. 9.2e-47;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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US-10-959-318-10
Query Match          93.7%; Score 543.5; DB 18; Length 110;
Best Local Similarity 93.6%; Pred. No. 1e-45;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY      1 APPVA-GPSVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 APPVAGSPSVFLPPPKDFTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      60 PREEQNSTFRVVSVLTVVHQDLWLNKGEYCKVSNKGLPSSIEKTIKTK 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 PREEQNSTFRVVSVLTVLHQDLWLNKGEYCKVSNKGLPSSIEKTIKSKAK 110
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-10-959-318-15
; Sequence 15, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and d (D268)
US-10-959-318-15

Query Match          93.1%; Score 540; DB 18; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.2e-45;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 APPVAGSPSVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 APPVAGSPSVFLPPPKDFTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 REEQNSTFRVVSVLTVVHQDLWLNKGEYCKVSNKGLPSSIEKTIKTK 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 REEQNSTFRVVSVLTVLHQDLWLNKGEYCKVSNKALPAPIEKTISKAK 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-959-318-16
; Sequence 16, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 109

```

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-16

Query Match      93.1%; Score 540; DB 18; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.2e-45;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP 60

QY 61 REQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 61 REQFNSTFRVSVLTVLHQDMLNGKEYCKVSNKGLPAPIEKTIISKAK 109

RESULT 10
US-11-018-102-25
; Sequence 25, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018,102
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: engineered G4 CH2
US-11-018-102-25

Query Match      92.8%; Score 538.5; DB 20; Length 110;
Best Local Similarity 93.6%; Pred. No. 3.1e-45;
Matches 103; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 APPVA-GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59
Db 1 APEAAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60

QY 60 PREEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 61 PREEQFNSTFRVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110

RESULT 11
US-10-267-286A-4
; Sequence 4, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/10/267,286A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
; OTHER INFORMATION: Peptide
US-10-267-286A-4

Query Match      92.4%; Score 536; DB 14; Length 109;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63
Db 4 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPRE 63

QY 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 64 QFNSTFRVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTIISKAK 109

RESULT 12
US-10-959-318-4
; Sequence 4, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-4

Query Match      92.4%; Score 536; DB 18; Length 110;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63
Db 5 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPRE 64

QY 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 65 QFNSTFRVSVLTVLHQDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110

RESULT 13
US-10-959-318-21
; Sequence 21, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
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; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG4 CH2 sequence with delta e (E368) mutation
US-10-959-318-21

Query Match 92.4%; Score 536; DB 18; Length 110;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE 63
Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSEDEPEVQFNWYVDGVEVHNAKTKPRE 64
Qy 64 QFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QFNSTFRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKSKAK 110

RESULT 14

US-11-018-102-24
; Sequence 24, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018,102
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-018-102-24

Query Match 92.4%; Score 536; DB 20; Length 110;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE 63
Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSEDEPEVQFNWYVDGVEVHNAKTKPRE 64
Qy 64 QFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QFNSTFRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKSKAK 110

RESULT 15

US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 19-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
US-10-959-318-13

Query Match 91.3%; Score 529.5; DB 18; Length 110;
Best Local Similarity 90.9%; Pred. No. 2.4e-44;
Matches 100; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
Qy 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
Db 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVDVSEDEPEVQFNWYVDGVEVHNAKTK 60
Qy 60 PREEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 PREEQFNSTFRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKSKAK 110

Search completed: November 17, 2005, 08:18:46
Job time : 83.3721 secs

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 91.6667 Seconds
(without-alignments)
464.112 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGSVFLPPKPKDT.....CKVSNKGLPSSIEKTIISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	98.1	110	3	AAY54998 Mutated C
2	570.5	97.2	109	3	AAY54996 Mutated C
3	570	97.1	435	7	Adm33857 Human HuE
4	570	97.1	435	8	Adm33857 Human HuE
5	570	97.1	447	7	Adm33380 Human GCS
6	562	95.7	468	2	Aaw85689 D9D10 hea
7	562	95.7	488	3	Aay97175 Human FGF
8	562	95.7	497	3	Aay97174 Human FGF
9	562	95.7	525	3	Aay97173 Human FGF
10	562	95.7	711	2	Aaw85692 MotABII f
11	561	95.6	447	6	Aae33524 Human AQC
12	560	95.4	251	6	Aae33523 Human imm
13	558	95.1	232	5	AB881492 Human mut
14	558	95.1	232	5	AB881491 Human mut
15	558	95.1	250	6	Aae35220 Human mod
16	558	95.1	251	2	Aay05688 Modified
17	558	95.1	251	2	Aaw97756 Modified
18	558	95.1	251	3	AB07541 Amino aci
19	558	95.1	251	6	Aae35218 Human mod
20	558	95.1	251	6	Aae35219 Human imm
21	558	95.1	328	5	AB881493 Ztnfr12-t
22	558	95.1	332	6	Aae35228 Human TAC
23	558	95.1	344	6	Aae35224 Human TAC
24	558	95.1	348	6	Aae35225 Human TAC
25	558	95.1	357	6	Aae35226 Human TAC

ALIGNMENTS

RESULT 1

AAY54998
ID AAY54998 standard; protein; 110 AA.

XX AC AAY54998;

XX 17-FEB-2000 (first entry)

XX DE Mutated CH2 sequence Gideltaac.

XX KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmunity thrombocytopenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion.

XX OS Synthetic.

XX PN WO9958572-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001441.

XX PR 08-MAY-1998; 98GB-00009951.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PI Armour KL, Clark MR, Williamson LM;

XX DR WPI; 2000-039075/03.

XX PT Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

XX PS Claim 12; Fig 17; 81pp; English.

XX CC This sequence represents the mutated CH2 molecule Gideltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC molecule is used to bind a target molecule (especially FcγmαRIIb
CC causing inhibition of B cell activation, mast cell degranulation or
CC phagocytosis). The binding molecule can be used to prevent or inhibit the
CC binding of a second binding molecule, e.g. an antibody, to the target
CC molecule. The binding molecule is useful for the treatment of graft-vs-
CC host disease, organ transplant rejection, bone-marrow transplant
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC coronary artery occlusion). The binding molecules do not activate
CC complement or trigger cytotoxic activities through FcγmαRIIb and desirable
CC IgG properties have been retained. The polypeptides do not contain non-
CC human amino acids, and are therefore likely to have reduced
CC immunogenicity. Further, they still bind Protein A, which is consistent
CC with being able to cross the human placenta through interaction with FcRn
CC (neonatal Fc receptor)
CC
CC
SQ Sequence 110 AA;

Query Match 98.1%; Score 576; DB 3; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.4e-51;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Qy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

RESULT 2
AA54996
ID AA54996 standard; protein; 109 AA.
XX
XX AA54996;
XX
DT 17-FEB-2000 (first entry)
DE
DE Mutated CH2 sequence Gideltaab.
XX
KW Binding molecule; CH2 sequence; complement dependent lysis; FcγmαRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmunity disease; asthma; allergy;
KW alloimmune disorder; autoimmunity haemolytic anaemia; inflammatory disease;
KW autoimmunity thrombocytopenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
OS Synthetic.
XX
XX WO958572-A1.
PN
XX
PD 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB001441.
XX
XX 08-MAY-1998; 98GB-00009951.
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
PA
XX
PI Armour KL, Clark MR, Williamson LM;
XX
XX WPI; 2000-039075/03.
XX
XX Immunoglobulin-derived binding molecules that do not activate complement
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.
XX
PS Claim 12; Fig 17; 81pp; English.
XX
CC This sequence represents the mutated CH2 molecule Gideltaab, and is a
CC binding molecule of the invention. The recombinant binding molecule is
CC capable of binding a target molecule without triggering complement
CC dependent lysis, or the cell-mediated destruction of the target
CC host disease, organ transplant rejection, bone-marrow transplant
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC coronary artery occlusion). The binding molecules do not activate
CC complement or trigger cytotoxic activities through FcγmαRIIb and desirable
CC IgG properties have been retained. The polypeptides do not contain non-
CC human amino acids, and are therefore likely to have reduced
CC immunogenicity. Further, they still bind Protein A, which is consistent
CC with being able to cross the human placenta through interaction with FcRn
CC (neonatal Fc receptor)
CC
CC
SQ Sequence 109 AA;
Query Match 97.2%; Score 570.5; DB 3; Length 109;
Best Local Similarity 99.1%; Pred. No. 5.3e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Qy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 60 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 109
RESULT 3
ADM33857
ID ADM33857 standard; protein; 435 AA.
XX
XX ADM33857;
AC
DT 03-JUN-2004 (first entry)
XX
DE Human HuEPO-L-vFcγmαRII fusion protein.
XX
XX
KW Erythropoietin; EPO; immunoglobulin; IgG;
KW fragment crystallisation region; Fc; chronic anaemia; renal disease;
KW cancer chemotherapy; rheumatoid arthritis; AIDS;
KW myelodysplastic syndrome; (HuEPO)-L-vFcγmαRII; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /note= "Signal peptide"
FT Protein 28..192
FT /note= "EPO"
FT Peptide 193..208
FT /note= "Linker"
FT Protein 209..435
FT /note= "IgG1 Fc"
FT Misc-difference 222

FT Misc-difference 318 /note= "Wild-type Leu substituted by Val"
FT /note= "Wild-type Leu substituted by Ala"
PN US2003082749-A1.
XX 01-MAY-2003.
XX 17-AUG-2001; 2001US-00932812.
XX 17-AUG-2001; 2001US-00932812.
XX (SUNL/) SUN L K.
PA (SUNB/) SUN B N C.
PA (SUNC/) SUN C R Y.
XX Sun LK, Sun BNC, Sun CRY;
XX WPI; 2003-616080/58.
DR N-PSDB; ADM33856.
XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for
PT treating patients with chronic anemia caused by renal failure, cancer
PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
PT infection.
XX Claim 5; Fig 2C; 14pp; English.
XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
CC fusion protein comprising HuEPO, a peptide linker, and a human
CC immunoglobulin G Fc (fragment crystallisation region) variant. Also
CC included is a carbohydrate-derived cell line producing the human
CC erythropoietin-L-vFc fusion protein cited above in its growth medium in
CC excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
CC -L-vFc fusion protein exhibits an enhanced in vitro biological activity
CC of at least 2-fold relative to that of recombinant HuEPO on a molar
CC basis. The flexible peptide linker containing about 20 or fewer amino
CC acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
CC contains amino acid mutations to attenuate effector functions. The human
CC IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
CC Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
CC human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The
CC recombinant human erythropoietin-L-vFc fusion proteins are useful for
CC treating patients with chronic anaemia caused by renal failure, cancer
CC chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
CC infection, or myelodysplastic syndrome. The increased activity and
CC prolonged presence of the human erythropoietin-L-vFc fusion protein in
CC the serum, as compared to prior art, leads to lower dosages and less
CC frequent injections. Less fluctuations of the drug in serum
CC concentrations means improved safety and tolerability, and less frequent
CC injections result in better patient compliance and quality of life. The
CC present sequence represents the fusion protein HuEPO-L-vFc_{gamma}1.
XX Sequence 435 AA;
SQ
Query Match 97.1%; Score 570; DB 7; Length 435;
Best Local Similarity 97.3%; Pred. No. 3.2e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 APPVAGGSPVFLPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 219 APEVAGGSPVFLPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278
QY 61 PREEQYNSTYRVVSVLTVLHQDLNGLKEYCKVKSNGKLPSPSTIEKTIISAK 110
Db 279 PREEQYNSTYRVVSVLTVLHQDLNGLKEYCKVKSNGKLPSPSTIEKTIISAK 328
RESULT 4
ADR48988
ID ADR48988 standard; protein; 435 AA.
XX
AC ADR48988;

XX 02-DEC-2004 (first entry)
XX HuEPO-L-vFc fusion protein #2.
XX antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
XX Homo sapiens.
OS Synthetic.
XX US2004175824-A1.
XX 09-SEP-2004.
XX 21-JAN-2004; 2004US-00761593.
XX 17-AUG-2001; 2001US-00932812.
XX (SUNL/) SUN L K.
PA (SUNB/) SUN B N C.
PA (SUNC/) SUN C R Y.
XX Sun LK, Sun BNC, Sun CRY;
XX WPI; 2004-634851/61.
DR N-PSDB; ADR48987.
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
PT (HuEPO), a peptide linker, and a human IgG Fc variant, useful for
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or
PT rheumatoid arthritis.
XX Claim 5; SEQ ID NO 22; 31pp; English.
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
CC (HuEPO), a peptide linker, and a human IgG Fc variant, is new.
CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster
CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
CC its growth medium in excess of 10 μ microg per million cells in a 24 hour
CC period; and a method for making a recombinant fusion protein comprising
CC HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred
CC Protein: The peptide linker containing 20 or fewer amino acids is present
CC between HuEPO and the human IgG Fc variant, and comprises two or more
CC amino acids selected from glycine, serine, alanine, and threonine. The
CC human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human
CC IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1
CC with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino
CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
CC biological activity similar to or higher than that of HuEPO on a molar
CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line
CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess
CC of 30 μ microg per million cells in a 24 hour period. The human IgG Fc
CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from
CC IgB1 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
CC the IgG Fc contains amino acid mutations to attenuate effector functions,
CC a flexible peptide linker containing 20 or fewer amino acids is present
CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion
CC protein exhibits in vitro biological activity similar to or higher than
CC that of HuEPO on a molar basis. Preferred Method: Making a recombinant
CC fusion protein comprising HuEPO, a flexible peptide linker, and a human
CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the
CC cell line where the recombinant protein is expressed in its growth medium
CC in excess of 10 μ microg per million cells in a 24 hour period; and
CC purifying the expressed protein from (b), where the recombinant fusion
CC protein exhibits in vitro biological activity similar to or higher than
CC that of HuEPO on a molar basis. Antianemic; Nephrotropic. No biological
CC data given. None given. Administration can be through subcutaneous or
CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion

CC protein is useful for treating patients with chronic anemia due to renal
 CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for
 CC HIV infection, or myelodysplastic syndrome. It is also useful in the
 CC treatment of renal failure. A fusion protein was assembled from several
 CC DNA segments. To obtain the gene encoding the leader peptide and mature
 CC protein of human erythropoietin (EPO), cDNA library of human fetal liver
 CC or kidney was used as the template in polymerase chain reaction (PCR).
 CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a
 CC restriction enzyme cleavage site is used as the 5' oligonucleotide
 CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon
 CC and incorporates a BamHI site. The resulting DNA fragments of
 CC approximately 600 bp were inserted into a holding vector such as pUC19 at
 CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the
 CC human EPO gene was confirmed by DNA sequencing.

XX SQ Sequence 435 AA;

Query Match 97.1%; Score 570; DB 8; Length 435;
 Best Local Similarity 97.3%; Pred. No. 3.2e-50;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 219 APEVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

DB 279 PREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPASIEKTIKAK 328

RESULT 5

ADM33380
 ID ADM33380 standard; protein; 447 AA.

XX ADM33380;

DT 03-JUN-2004 (first entry)

DE Human GCSF-L-fragment of crystallisation gamma 1 fusion protein.

XX cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;
 KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vfc;
 KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;
 KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;
 KW bone marrow transplantation; chronic neutropenia; fusion protein;
 KW fragment of crystallisation gamma 1; FC gamma 1.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 234 /note= "Wild type Leu substituted by Val"

FT Misc-difference 235 /note= "Wild type Leu substituted by Ala"

FT Misc-difference 331 /note= "Wild type Pro substituted by Ser"

XX US2003082679-A1.

XX 01-MAY-2003.

XX 01-OCT-2001; 2001US-00968362.

XX 01-OCT-2001; 2001US-00968362.

XX (SUNL/) SUN L K.

XX (SUNB/) SUN B N C.

XX (SUNC/) SUN C R Y.

XX Sun LK, Sun BNC, Sun CRY;

XX WPI; 2003-585400/55.

DR N-PSDB; ADM33379.

XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-
 FT vfc fusion protein for treating immune or hematopoietic system disorders
 FT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G
 FT FC variant.

XX Disclosure; Fig 2C; 15pp; English.

XX The invention describes a recombinant human granulocyte colony-
 CC stimulating factor (hG-CSF)-L-vfc fusion protein comprising hG-CSF, a
 CC peptide linker, and a human immunoglobulin G (IgG) FC variant. Also
 CC described are: a CHO-derived cell line producing the above hG-CSF-L-vfc
 CC fusion protein in its growth medium in excess of 10 mg/grg per million
 CC cells in a 24-hour period; and making the recombinant fusion protein.
 CC cited above, comprising generating a CHO-derived cell line cited above,
 CC growing the cell line under conditions the recombinant fusion protein is
 CC expressed in its growth medium, and purifying the expressed protein. The
 CC recombinant fusion protein is useful in treating a variety of conditions
 CC associated with an impaired immune or hematopoietic system, including
 CC cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow
 CC transplantation, and chronic neutropenias. This is the amino acid
 CC sequence of human GCSF-L-fragment of crystallisation gamma 1 variant
 CC fusion protein.

XX SQ Sequence 447 AA;

Query Match 97.1%; Score 570; DB 7; Length 447;

Best Local Similarity 97.3%; Pred. No. 3.3e-50;

Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

DB 231 APEVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

DB 291 PREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPASIEKTIKAK 340

RESULT 6

AAW85689

ID AAW85689 standard; protein; 468 AA.

XX AAW85689;

DT 12-AUG-1999 (first entry)

DE D9D10 heavy chain fusion protein.

XX Antibody; humanised; variable region; heavy chain; light chain;
 KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
 KW immune disease; multiple sclerosis; Crohn's disease; skin disorders;
 KW inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
 KW multivalent; ruminant.

OS Synthetic.

OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..20

FT /note= "D9D10 light chain signal peptide"

FT Domain 21..137

FT /note= "Humanised heavy chain variable domain of D9D10"

FT Domain 138..467

FT /note= "Human IgG1 heavy chain constant domain"

FT Misc-difference 468

FT /note= "Leu added by cloning strategy"

XX WO9909055-A2.

XX 25-FEB-1999.


```

XX SQ Sequence 488 AA;
Query Match 95.7%; Score 562; DB 3; Length 488;
Best Local Similarity 95.5%; Pred. No. 2.5e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 APPVAGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 272 APELEGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331
Oy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 332 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 381

RESULT 8
AA97174
ID AA97174 standard; protein; 497 AA.
XX AC AA97174;
XX DT 04-DEC-2000 (first entry)
XX DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.
XX KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnery;
KW ophthalmological; anti-proliferative.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FH Peptide 1..21
FT /label= FGF-R1_signal_peptide
FT Domain 22..257
FT /label= FGF-R1_extracellular_domain
FT /note= "The Ig I segment and acid box are deleted"
FT Domain 59..111
FT /label= Ig_II_segment
FT Domain 157..222
FT /label= Ig_III_segment
FT Peptide 258..265
FT /label= Linker
FT Region 266..497
FT /label= Human IgG1 Fc region
FT /note= "Contains hinge region and domains CH2 and CH3"
FT Misc-difference 285
FT /label= L285E
FT /note= "This mutation decreases the affinity of the Fc
FT portion for Fc receptors"
FT Misc-difference 385
FT /label= P385S
FT /note= "This mutation decreases the affinity of the Fc
FT portion for complement"
XX PN WO200046380-A2.
XX PD 10-AUG-2000.
XX PF 07-FEB-2000; 2000WO-US003166.
XX PR 08-FEB-1999; 99US-0119002P.
XX PA (CHIR ) CHIRON CORP.
XX PI Kavanaugh WM, Ballinger M;
XX DR WPI; 2000-514961/46.
XX DR N-PSDB; AAA52131.
XX PT New polypeptide comprising a fibroblast growth factor receptor
extracellular domain fused to a heterologous oligomerization domain for
treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
Claim 14; Page 65-66; 70pp; English.
Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
(Ig) I segment fused to a heterologous oligomerization domain that
comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
region, or light chain of an immunoglobulin molecule, or a peptide with a
leucine zipper motif. The Ig I segment is not necessary for binding of
acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
affinity for aFGF and heparin, protects the core of the molecule from
proteolysis, and abrogates the heparin requirement for aFGF binding. The
new fusion polypeptides are better FGF inhibitors than FGF-R monomer
proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at
subnanomolar concentrations and were 20-fold more potent than the FGF-R
monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung,
rectal, testis and cervical tumours), neovascularization (e.g. diabetic
retinopathy, neovascular glaucoma, wound healing and corneal scarring)
and hyper-proliferation of vascular smooth muscle cells (e.g.
postangioplasty and postatherectomy restenosis)
XX SQ Sequence 497 AA;
Query Match 95.7%; Score 562; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.5e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 APPVAGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 281 APELEGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340
Oy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 341 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 390

RESULT 9
AA97173
ID AA97173 standard; protein; 525 AA.
XX AC AA97173;
XX DT 04-DEC-2000 (first entry)
XX DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.
XX KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnery;
KW ophthalmological; anti-proliferative.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FH Peptide 1..21
FT /label= FGF-R1_signal_peptide
FT Domain 22..285
FT /label= FGF-R1_extracellular_domain
FT /note= "Ig I segment is deleted"
FT Domain 37..44
FT /label= Acid_box_segment
FT Domain 87..139
FT /label= Ig_II_segment
FT Peptide 286..293
FT /label= Linker
FT Region 294..525
FT /label= Human IgG1_Fc_region
FT /note= "Contains hinge region and domains CH2 and CH3"
FT Misc-difference 313

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Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0									
QY	1	APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60							
Db	232	APEAAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 291							
QY	61	PREEQNSTYRVSVLTVLHQDWLNGKEYKCKVKNKGLPSSIEKTIKAK 110							
Db	292	PREEQNSTYRVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTIKAK 341							
RESULT 12									
AAE35231									
ID	AAE35231	standard; protein; 251 AA.							
XX	AAE35231;								
AC	AAE35231;								
XX	28-MAY-2003 (first entry)								
DT		Human immunoglobulin gammal mutant protein, A134S.							
DE									
XX									
XX		Transmembrane activator; calcium modulator; nephrotropic; antibacterial;							
KW		TAC1; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;							
KW		anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;							
KW		glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;							
KW		dermatological; neuroprotective; cyclophilin ligand-interactor; human;							
KW		autoimmune disease; systemic lupus erythematosus; multiple sclerosis;							
KW		diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;							
KW		mutant; mutein.							
XX									
OS		Homo sapiens.							
OS		Synthetic.							
XX									
FX	Key	Location/Qualifiers							
FT	Binding-site	38..41							
FT		/note= "FcgammaRI binding site"							
FT	Misc-difference	134							
FT		/note= "Wild-type Ala is replaced with Ser"							
XX									
PN	W0200294852-A2.								
XX									
PD	28-NOV-2002.								
XX									
PF	20-MAY-2002; 2002WO-US015910.								
XX									
PR	24-MAY-2001; 2001US-0293343P.								
XX		(ZYMO) ZYMOGENETICS INC.							
PA									
XX		Rixon MW, Gross JA;							
PI									
XX		WPI; 2003-148455/14.							
DR									
XX									
XX		Transmembrane activator and calcium modulator and cyclophilin ligand-							
PT		interactor (TAC1)-immunoglobulin fusion protein, for treating cancer or							
PT		diabetes, comprises a TAC1 receptor group and an immunoglobulin group.							
XX									
PS		Example 1; Col; 71pp; English.							
XX									
CC		The invention relates to fusion proteins comprising transmembrane							
CC		activator and calcium modulator and cyclophilin ligand-interactor (TAC1)							
CC		receptor group that binds tumour necrosis factor-like protein (ZTNF2) or							
CC		ZTNF4; and an immunoglobulin group comprising a constant region of an							
CC		immunoglobulin. The invention is used to manufacture a medicament for							
CC		inhibiting the proliferation of tumour cells in a mammalian subject. The							
CC		composition comprising the fusion protein may also be used in treating							
CC		autoimmune diseases (e.g. systemic lupus erythematosus, multiple							
CC		sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal							
CC		diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft							
CC		rejection, anaemia and septic shock. The fusion proteins are also used in							
CC		gene therapy. The present sequence is human immunoglobulin gammal mutant							
CC		protein. This sequence is used in the exemplification of the invention.							
CC		Note: This sequence is not shown in the specification, however it is							

AAE33524																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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CC constructed based on human immunoglobulin gammal protein (SEQ ID NO:6)
 CC sequence shown in column 92-93 (AAE35214)
 XX
 SQ Sequence 251 AA;

Query Match 95.4%; Score 560; DB 6; Length 251;
 Best Local Similarity 95.5%; Pred. No. 1.8e-49;
 Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db |||||
 35 APELLGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94
 |||||

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 Db |||||
 95 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 144
 |||||

RESULT 13
 ABB81492
 ID ABB81492 standard; protein; 232 AA.
 XX
 AC ABB81492;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Human mutated Fc protein designated Fc5 SEQ ID NO:32.
 XX

Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 light chain neuropathy; hypertension; large vessel disease;
 graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200238766-A2.
 PN
 XX 16-MAY-2002.
 PD
 XX
 XX 05-NOV-2001; 2001WO-US047018.
 XX
 XX 07-NOV-2000; 2000US-0246449P.
 PR
 XX 20-DEC-2000; 2000US-0257131P.
 PR
 XX 28-JUN-2001; 2001US-0301715P.
 PR
 XX 29-AUG-2001; 2001US-0315565P.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 FI
 XX WPI; 2002-508212/54.
 XX
 DR N-PSDB; ABN8947.
 DR
 XX

Novel isolated human tumor necrosis factor receptor polypeptide, termed
 Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
 renal failure or renal disease and lymphoma.

Example 4; Page 148-149; 154pp; English.

The present invention describes a human tumour necrosis factor receptor
 designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 dermatological, antiinflammatory, neuroprotective, antidiabetic,
 antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 activities, and can be used in gene therapy. (I) can be used for
 inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12

(e.g. ZTNF4), for treating disorders and diseases associated with B
 lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 inhibiting the proliferation of tumour cells. (I) is useful for treating
 autoimmune disorders such as systemic lupus erythematosus, myasthenia
 gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 leukaemia, nephritis, and pyelonephritis, and for treating renal
 neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 amyloidosis, hypertension, large vessel diseases, graft-versus host
 disease, graft rejection and Crohn's disease. (I) is useful for
 modulating the immune system, for regulating B cell responses and
 development, for modulating development of other cells, antibody
 production and cytokine production, and for modulating T and B cell
 communication. Human Ztnfr12 is located to chromosome 22q13.2. The
 present sequence represents a mutated Fc protein designated Fc5, which is
 used in an example from the present invention

XX Sequence 232 AA;
 SQ

Query Match 95.1%; Score 558; DB 5; Length 232;
 Best Local Similarity 95.5%; Pred. No. 2.6e-49;
 Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db |||||
 16 APEAGAPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
 |||||

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 Db |||||
 76 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 125
 |||||

RESULT 14
 ABB81491
 ID ABB81491 standard; protein; 232 AA.
 XX
 AC ABB81491;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Human mutated Fc designated Fc4 protein SEQ ID NO:28.
 XX

Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 light chain neuropathy; hypertension; large vessel disease;
 graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200238766-A2.
 PN
 XX 16-MAY-2002.
 PD
 XX
 XX 05-NOV-2001; 2001WO-US047018.
 XX
 XX 07-NOV-2000; 2000US-0246449P.
 PR
 XX 20-DEC-2000; 2000US-0257131P.
 PR
 XX 28-JUN-2001; 2001US-0301715P.
 PR
 XX 29-AUG-2001; 2001US-0315565P.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 FI
 XX WPI; 2002-508212/54.
 XX
 DR N-PSDB; ABN8947.
 DR
 XX

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DR WPI; 2002-508212/54.
DR N-PSDB; AEN89444.
XX
XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Znf12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
XX Example 4; Page 146; 154pp; English.
XX
XX The present invention describes a human tumor necrosis factor receptor
CC designated Znf12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Znf12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. Human Znf12 is located to chromosome 22q13.2. The
CC present sequence represents a mutated Fc protein designated Fc4, which is
CC used in an example from the present invention
XX
XX Sequence 232 AA;
SQ
Query Match 95.1%; Score 558; DB 5; Length 232;
Best Local Similarity 95.5%; Pred. No. 2.6e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 16 APEAGAPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 125
RESULT 15
AAE35220
ID AAE35220 standard; protein; 250 AA.
XX
XX AAE35220;
AC
XX
XX
XX 28-MAY-2003 (first entry)
DE Human modified immunoglobulin moiety #3.
XX
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW TACT; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200294852-A2.
XX
XX 28-NOV-2002.
XX

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PF 20-MAY-2002; 2002WO-US015910.
XX
XX 24-MAY-2001; 2001US-0293343P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Rixon MW, Gross JA;
PI
XX
XX WPI; 2003-148455/14.
DR N-PSDB; AAD53758.
XX
XX Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
XX Disclosure; Col 110-111; 71pp; English.
XX
XX The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human modified immunoglobulin
CC moiety used in the invention
XX
XX Sequence 250 AA;
SQ
Query Match 95.1%; Score 558; DB 6; Length 250;
Best Local Similarity 95.5%; Pred. No. 2.8e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 35 APEAGAPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 144
Search completed: November 17, 2005, 07:04:55
Job time : 92.6667 secs

```


Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	557	94.9	234	2	PT0207	IG gamma chain C r
2	557	94.9	255	4	S31866	IG gamma-1 chain C
3	557	94.9	330	1	GHU	IG gamma-1 chain C
4	557	94.9	374	2	S69339	IG heavy chain V r
5	553	94.2	327	1	G4HU	IG gamma-4 chain C
6	543.5	92.6	326	1	G2HU	IG gamma-2 chain C
7	539	91.8	377	2	A23511	IG gamma-2 chain C
8	539	91.8	377	2	A60764	IG gamma-3 chain C
9	519	88.4	289	1	G3HUVI	IG gamma-3 chain C
10	458	78.0	328	2	I47160	IG gamma-3 heavy c
11	458	78.0	328	2	I47159	IG gamma 2a chain
12	453	77.2	277	2	I47162	IG gamma 2a chain
13	440	75.0	470	2	S22080	IG heavy chain pre
14	434	73.9	328	2	I47161	IG gamma 3 chain c
15	434	73.9	328	2	I47158	IG gamma 1 chain c
16	431	73.4	333	2	PS0018	IG gamma-2b chain
17	421	71.7	308	2	C30554	IG heavy chain C r
18	421	71.7	323	1	GHRB	IG gamma chain C r
19	421	71.7	329	1	G2GP	IG gamma-2 chain C
20	421	71.7	472	2	S31459	IG gamma-1 chain
21	418	71.2	329	1	G3MSC	IG gamma-3 chain C
22	418	71.2	398	1	G3MSC	IG gamma-3 chain C
23	410	69.8	327	2	S05611	IG gamma-2 chain C
24	397	67.6	405	1	G2MSBM	IG gamma-2b chain
25	397	67.6	474	1	G2MSB11	IG gamma-2b chain
26	396	67.5	324	1	G1MS	IG gamma-1 chain C
27	396	67.5	329	2	S00847	IG gamma-2c chain
28	396	67.5	393	1	G1MSM	IG gamma-1 chain C
29	396	67.5	444	2	PC4436	monoclonal antibody

Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 60
|| : |||||
Db 39 APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 98
|| : |||||
QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
|| : |||||
Db 99 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
|| : |||||

RESULT 3
GHU
Ig gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R/Elison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A/Reference number: A93433; MUID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA
A/Residues: 1-330 <ELL>
A/Cross-references: UNIPROT:P01857; EMBL:Z17370
A/Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers,
A/Note: Lys-330 is removed after translation
R/Harris, L.J.
submitted to the EMBL Data Library, October 1992
A/Reference number: S33904
A/Accession: S36861
A/Molecule type: DNA
A/Residues: 2-330 <HAR>
A/Cross-references: EMBL:Z17370
R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A/Reference number: S33887; MUID:83001943; PMID:6811139
A/Accession: S33887
A/Molecule type: DNA
A/Residues: 88-113;235-330 <TAK>
A/Cross-references: EMBL:Z17370
R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A/Reference number: A90563; MUID:71064024; PMID:5489771
A/Contents: myeloma protein Eu
A/Accession: B90563
A/Molecule type: Protein
A/Residues: 1-96, R',98-135 <GUN>
A/Note: this sequence has the Gm(3) marker, 97-Arg
R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A/Reference number: A90564; MUID:71064025; PMID:5530842
A/Contents: Eu
A/Accession: A90564
A/Molecule type: Protein
A/Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A/Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met
R/Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie).
igen Primärstruktur.
A/Reference number: A91668; MUID:77070269; PMID:826475
A/Contents: myeloma protein Nie
A/Accession: B91668
A/Molecule type: protein
A/Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A/Note: this sequence has the Gm(17) and Gm(1) markers
R/Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A/Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A/Reference number: A91723; MUID:83289131; PMID:6884994

A/Contents: myeloma protein KOL; disulfide bonds
A/Accession: A91723
A/Molecule type: protein
A/Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A/Note: this sequence has the Gm(3) and Gm(non-1) markers
R/Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A/Reference number: A90565; MUID:71064027; PMID:4923144
A/Contents: annotation; disulfide bonds
R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobuli
enbromide cleavage products, and the disulfide bridges.
A/Reference number: A91667; MUID:77070267; PMID:1002129
A/Contents: annotation; disulfide bonds
C/Genetics:
A/Gene: GDB:IGHG1
A/Cross-references: GDB:120085; OMIM:147100
A/Map position: 14q32.33-14q32.33
A/Introns: 99/1; 114/1; 224/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IMI>
F/137-206/Domain: immunoglobulin homology <IM2>
F/243-310/Domain: immunoglobulin homology <IM3>
F/27-83,144-204,250-308/Disulfide bonds: #status experimental
F/103/Disulfide bonds: interchain (to light chain) #status experimental
F/109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F/180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 94.9%; Score 557; DB 1; Length 330;
Best Local Similarity 94.5%; Pred. No. 2.1e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 60
|| : |||||
Db 114 APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 173
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
|| : |||||
Db 174 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
|| : |||||

RESULT 4
S69339
Ig heavy chain V region precursor - human
C/Species: Homo sapiens (man)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C/Accession: S69339; S72664
R/Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A/Reference number: S69339; MUID:95262687; PMID:7744049
A/Accession: S69339
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-374 <KHA>
A/Cross-references: EMBL:X81695
R/Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A/Reference number: S72664
A/Accession: S72664
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140,'C',142-374 <KH2>
A/Cross-references: EMBL:X81695
C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 94.9%; Score 557; DB 2; Length 374;
Best Local Similarity 94.5%; Pred. No. 2.4e-47;

Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 158 APELLGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217
 Qy 61 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 110
 Db 218 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPAPIEKTISKAK 267

RESULT 5
 G4HU
 Ig gamma-4 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 C:Accession: A90933; A90249; A02150
 R:Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A:Reference number: A90933; MUID:83157104; PMID:6299662
 A:Accession: A90933
 A:Molecule type: DNA
 A:Residues: 1-327 <ELL>
 A:Cross-references: UNIPROT:P01861
 A:Note: the sequence was determined from the germline gene
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
 A:Reference number: A90249; MUID:70207560; PMID:4192699
 A:Accession: A90249
 A:Molecule type: protein
 A:Residues: 1-30; 81-326 <PIN>
 C:Genetics:
 A:Gene: GDB:IGHG4
 A:Cross-references: GDB:119340; OMIM:147130
 A:Map position: 14q32.33-14q32.33
 A:Introns: 99/1; 111/1; 221/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:99-110/Region: hinge
 F:134-203/Domain: immunoglobulin homology <IM2>
 F:240-307/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83, 141-201, 247-305/disulfide bonds: #status predicted
 F:106, 109/disulfide bonds: interchain (to heavy chain) #status experimental
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.2%; Score 553; DB 1; Length 327;
 Best Local Similarity 94.5%; Pred. No. 5.1e-47;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 111 APELLGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 170
 Qy 61 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 110
 Db 171 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 220

RESULT 6
 G2HU
 Ig gamma-2 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
 C:Accession: A93906; A92809; A93132; A02148
 R:Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A:Reference number: A93906; MUID:82197621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein Til
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connel, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A:Note: this sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132
 A:Molecule type: protein
 A:Residues: 238-275 <HOF>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
 ned
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90253; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83, 140-200, 246-304/disulfide bonds: #status experimental
 F:102, 103, 106, 109/disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.6%; Score 543.5; DB 1; Length 326;
 Best Local Similarity 92.7%; Pred. No. 4.4e-46;
 Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 111 APPVA-GPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 169
 Qy 61 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 110

C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
C;Genetics:
A;Gene: IGG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 458; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 1.2e-37;
Matches 82; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 7 GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQY 66
Db 116 GPSVFIFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQY 175

Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 176 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 219

RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
C;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C;Genetics:
A;Gene: IGG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 458; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 1.2e-37;
Matches 82; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 7 GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQY 66
Db 116 GPSVFIFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQY 175

Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 176 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 219

RESULT 12
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
C;Cross-references: EMBL:U03782; NID:9433129; PIDN:AAA52220.1; PID:9433130
C;Genetics:
A;Gene: IGG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 453; DB 2; Length 277;
Best Local Similarity 77.9%; Pred. No. 3.1e-37;
Matches 81; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy 7 GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQY 66
Db 65 GPSAFIFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQY 124

Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 125 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 168

RESULT 13
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.0%; Score 440; DB 2; Length 470;
Best Local Similarity 72.5%; Pred. No. 1.1e-35;
Matches 79; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 2 PPVAGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 253 PELPGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 312

Qy 62 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 313 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 361

RESULT 14
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

Search completed: November 17, 2005, 07:11:37
Job time : 18.0822 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 80.6164 Seconds
(without alignments)
698.725 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVLPFPKPKDT.....CKVSNKGLPSSIEKTIISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	94.9	330	1 GCL HUMAN	P01857 homo sapien
2	557	94.9	348	2 Q6PYX1	Q6PYX1 homo sapien
3	557	94.9	465	2 Q6GMX6	Q6GMX6 homo sapien
4	557	94.9	466	2 Q6IN78	Q6IN78 homo sapien
5	557	94.9	469	2 Q7Z7P5	Q7Z7P5 homo sapien
6	557	94.9	470	2 Q6PJ44	Q6PJ44 homo sapien
7	557	94.9	470	2 Q7Z5W1	Q7Z5W1 homo sapien
8	557	94.9	472	2 Q6N089	Q6N089 homo sapien
9	557	94.9	473	2 Q6MZV7	Q6MZV7 homo sapien
10	557	94.9	473	2 Q6P055	Q6P055 homo sapien
11	557	94.9	475	2 Q6GMW7	Q6GMW7 homo sapien
12	557	94.9	475	2 Q6MZ06	Q6MZ06 homo sapien
13	557	94.9	475	2 Q6N095	Q6N095 homo sapien
14	557	94.9	476	2 Q6GMX1	Q6GMX1 homo sapien
15	557	94.9	478	2 Q6PIB1	Q6PIB1 homo sapien
16	557	94.9	480	2 Q6N094	Q6N094 homo sapien
17	557	94.9	480	2 Q6PJF1	Q6PJF1 homo sapien
18	557	94.9	481	2 Q6N097	Q6N097 homo sapien
19	557	94.9	482	2 Q7Z351	Q7Z351 homo sapien
20	557	94.9	544	2 Q6PJ95	Q6PJ95 homo sapien
21	557	94.9	679	2 Q96PQ8	Q96PQ8 homo sapien
22	554	94.2	466	2 Q6N096	Q6N096 homo sapien
23	553	94.2	327	1 G4 HUMAN	P01861 homo sapien
24	553	94.2	473	2 Q8TC63	Q8TC63 homo sapien
25	552	94.0	487	2 Q85ZL2	Q85ZL2 mus sp. fv/
26	550	93.7	476	2 Q6MZX7	Q6MZX7 homo sapien
27	543.5	92.6	326	1 GCL HUMAN	P01859 homo sapien
28	543.5	92.6	317	2 Q6N093	Q6N093 homo sapien
29	543.5	92.6	465	2 Q6P6C4	Q6P6C4 homo sapien
30	540.5	92.1	464	2 Q6MZU6	Q6MZU6 homo sapien
31	539	91.8	354	2 Q86TT2	Q86TT2 homo sapien

32	539	91.8	518	2 Q6N030	Q6N030 homo sapien
33	535	91.1	509	2 Q8NF17	Q8NF17 homo sapien
34	535	91.1	521	2 Q8N4Y9	Q8N4Y9 homo sapien
35	534.5	91.1	493	2 Q68CN4	Q68CN4 homo sapien
36	519	88.4	290	1 GC3 HUMAN	P01860 homo sapien
37	458	78.0	337	2 Q95M34	Q95M34 equus caball
38	431	73.4	333	1 GCB_RAT	P20761 rattus norv
39	421	71.7	323	1 GC_RABIT	P01870 oryctolagus
40	421	71.7	329	1 GC2_CAVPO	P01862 cavia porce
41	418	71.2	303	2 Q6KAM2	Q6KAM2 mus musculu
42	418	71.2	329	1 GC3_MOUSE	P22436 mus musculu
43	418	71.2	398	1 GC3M_MOUSE	P03987 mus musculu
44	418	71.2	470	2 Q7TMK1	Q7TMK1 mus musculu
45	397	67.6	336	1 GCB_MOUSE	P01866 mus musculu

ALIGNMENTS

RESULT 1
GC1 HUMAN
ID GC1 HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=684994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;

RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RL Intrachain disulfide bonds.";
 RP Biochemistry 9:3188-3196(1970).
 RP [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RP [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC GIM(3) marker and the GLM (non-1) markers.
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
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 CC -----
 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1AJ7; X-ray; H=1-103.
 DR PDB; 1DSB; X-ray; B/H=1-101.
 DR PDB; 1DS1; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FC1; X-ray; A/B=106-329.
 DR PDB; 1FC2; X-ray; D=106-329.
 DR PDB; 1FCC; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I7Z; X-ray; B/D=1-103.
 DR PDB; 1IIS; X-ray; A/B=107-330.
 DR PDB; 1IIX; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1O0X; X-ray; A/B=119-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT 99 110 Hinge.

FT	DOMAIN	111	223	CH2.
FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	Interchain (with light chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	N-linked (GlcNAc. -).
FT	VARIANT	97	97	K -> R (in GIM(3) marker).
FT				/FTId=VAR_003886.
FT				D -> E (in GIM(non-1) marker).
FT	VARIANT	239	239	/FTId=VAR_003887.
FT				L -> M (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTId=VAR_003888.
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	STRAND	176	177	
FT	TURN	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	TURN	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770BE106C2FA33D CRC64;

Query Match 94.9%; Score 557; DB 1; Length 330;
 Best Local Similarity 94.5%; Pred. No. 3.5e-47;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGSGPSVLPFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 ||: |||||
 DB 114 APELLGGPSVLPFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173


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QY 61 PREQYNSTYRVSVSLTLVHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB 174 PREQYNSTYRVSVSLTLVHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 223

RESULT 2
Q6PYX1 PRELIMINARY; PRT; 348 AA.
AC Q6PYX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -.
DR HSP; P01857; 1A7.
DR GO: 0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Receptor.
FT NON TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 348;
Best Local Similarity 94.5%; Pred. No. 3.8e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 132 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 191

QY 61 PREQYNSTYRVSVSLTLVHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB 192 PREQYNSTYRVSVSLTLVHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 241

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG-.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 94.9%; Score 557; DB 2; Length 465;
Best Local Similarity 94.5%; Pred. No. 5.2e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 249 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 308

QY 61 PREQYNSTYRVSVSLTLVHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB 309 PREQYNSTYRVSVSLTLVHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 358

RESULT 4
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.CI.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGCI; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;

Query Match 94.9%; Score 557; DB 2; Length 466;
Best Local Similarity 94.5%; Pred. No. 5.2e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 250 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 309

Qy 61 PREEQYNSTYRVSVLTVLDHQLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 310 PREEQYNSTYRVSVLTVLDHQLNGKEYCKVSNKALPAIEKTIKAK 359

RESULT 5
Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.CI.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8DSBE12BAAF795C CRC64;

Query Match 94.9%; Score 557; DB 2; Length 469;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 253 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 312

Qy 61 PREEQYNSTYRVSVLTVLDHQLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 313 PREEQYNSTYRVSVLTVLDHQLNGKEYCKVSNKALPAIEKTIKAK 362

RESULT 6
Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
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RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IG1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 470;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 254 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 314 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 363

RESULT 7
Q7Z5W1 ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marta M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;

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RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 94.9%; Score 557; DB 2; Length 470;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 254 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 314 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 363

RESULT 8
Q6N089 ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 472;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 256 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 315

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

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Db 316 PREEQNSTYRVVSVTLVLHODWLNKGKCKVSNKALPAPIEKTISKAK 365

RESULT 9
Q6MZV7 PRELIMINARY; PRT; 473 AA.
ID Q6MZV7;
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Peripheral Nervous System;
RC The German Human cDNA Consortium;
RG Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RL EMBL; BX640853; CAE45920.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4CBFC447 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 473;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFPPPKDGLMISRTPEVTVCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60
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Db 257 APILLGGPSVFLFPKPDKTLMISRTPEVTVCVVVDVSHEDPEVKFNWYVDGVEVHNATK 316
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Qy 61 PREEQNSTYRVVSVTLVLHODWLNKGKCKVSNKGLPSSIETIKTSKAK 110
||| : |||||
Db 317 PREEQNSTYRVVSVTLVLHODWLNKGKCKVSNKALPAPIEKTISKAK 366
||| : |||||

RESULT 10
Q6P055 PRELIMINARY; PRT; 473 AA.
ID Q6P055;
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Peripheral Nervous System;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1F5E5D736860F8 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 368

RESULT 12
Q6MZQ6
ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAB45972.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 368

RESULT 14
Q6GMX1
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DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7AE255A26F4B8E CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 368

RESULT 13
Q6N095
ID Q6N095 PRELIMINARY; PRT; 475 AA.
AC Q6N095;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686K03196.
GN Name=DKFZp686K03196;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640821; CAB45775.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 368

RESULT 14
Q6GMX1
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ID O6GMX1 PRELIMINARY; PRT; 476 AA.
 AC O6GMX1; 2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Rodriguez A.C., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RA EMBL; BC073773; AAH3773.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

 Query Match 94.9%; Score 557; DB 2; Length 476;
 Best Local Similarity 94.5%; Pred. No. 5.3e-47;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 260 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 319

 QY 61 PREEQNSTYRYVSVLTVLHODWLNCKEYKCKVSNKGLPSSIEKTSKAK 110
 Db 320 PREEQNSTYRYVSVLTVLHODWLNCKEYKCKVSNKGLPAPIEKTSKAK 369

 RESULT 15
 Q6PI81 PRELIMINARY; PRT; 478 AA.
 AC Q6PI81;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Rodriguez A.C., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RA EMBL; BC041037; AAH41037.1; -
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

 Query Match 94.9%; Score 557; DB 2; Length 478;
 Best Local Similarity 94.5%; Pred. No. 5.4e-47;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 262 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 321

 QY 61 PREEQNSTYRYVSVLTVLHODWLNCKEYKCKVSNKGLPSSIEKTSKAK 110
 Db 322 PREEQNSTYRYVSVLTVLHODWLNCKEYKCKVSNKGLPAPIEKTSKAK 371

 Search completed: November 17, 2005, 07:10:20
 Job time : 81.6164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.6119 Seconds
(without alignments)
333.636 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Issued Patents AA.*
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 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	97.1	447	4	US-09-968-362A-22
2	562	95.7	468	3	US-09-485-737B-67
3	562	95.7	468	4	US-10-071-485-67
4	562	95.7	488	4	US-09-499-846-12
5	562	95.7	497	4	US-09-499-846-10
6	562	95.7	525	4	US-09-499-846-8
7	562	95.7	711	3	US-09-485-737B-90
8	562	95.7	711	4	US-10-071-485-90
9	558	95.1	449	4	US-09-968-362A-20
10	558	95.1	559	4	US-09-746-359A-62
11	558	95.1	594	4	US-09-746-359A-23
12	557	94.9	110	3	US-08-444-644-21
13	557	94.9	110	3	US-08-232-246A-21
14	557	94.9	116	2	US-08-232-539D-55
15	557	94.9	212	1	US-08-430-633-4
16	557	94.9	212	2	US-08-620-694A-4
17	557	94.9	212	2	US-08-936-854-4
18	557	94.9	212	3	US-09-022-255-4
19	557	94.9	212	3	US-09-022-696-4
20	557	94.9	212	3	US-09-022-253-4
21	557	94.9	212	3	US-09-022-260-4
22	557	94.9	212	3	US-09-022-259-4
23	557	94.9	212	3	US-09-022-257-4
24	557	94.9	212	4	US-09-549-679-4
25	557	94.9	212	4	US-10-033-522-2
26	557	94.9	218	4	US-09-483-588-3
27	557	94.9	218	4	US-09-483-588-4

28	557	94.9	228	4	US-09-428-082B-2	Sequence 2, Appli
29	557	94.9	228	4	US-09-847-249A-2	Sequence 2, Appli
30	557	94.9	228	4	US-09-840-669B-2	Sequence 2, Appli
31	557	94.9	228	4	US-09-843-221A-2	Sequence 2, Appli
32	557	94.9	228	4	US-09-709-704A-2	Sequence 2, Appli
33	557	94.9	228	4	US-09-422-838C-5	Sequence 5, Appli
34	557	94.9	229	4	US-09-122-144-2	Sequence 2, Appli
35	557	94.9	232	2	US-08-595-043A-50	Sequence 50, Appli
36	557	94.9	232	4	US-09-968-362A-26	Sequence 26, Appli
37	557	94.9	235	3	US-09-131-247-6	Sequence 6, Appli
38	557	94.9	235	4	US-09-784-623-6	Sequence 6, Appli
39	557	94.9	243	4	US-09-428-082B-1068	Sequence 1068, Ap
40	557	94.9	247	4	US-09-428-082B-6	Sequence 6, Appli
41	557	94.9	247	4	US-09-428-082B-12	Sequence 12, Appli
42	557	94.9	248	4	US-09-428-082B-1056	Sequence 1056, Ap
43	557	94.9	248	4	US-09-428-082B-1058	Sequence 1058, Ap
44	557	94.9	248	4	US-09-428-082B-1060	Sequence 1060, Ap
45	557	94.9	248	4	US-09-428-082B-1062	Sequence 1062, Ap

ALIGNMENTS

RESULT 1

US-09-968-362A-22

; Sequence 22, Application US/09968362A

; Patent No. 6797493

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor

; TITLE OF INVENTION: increased biological activities

; FILE REFERENCE: 03SUN2001

; CURRENT APPLICATION NUMBER: US/09/968.362A

; CURRENT FILING DATE: 2001-10-01

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 22

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: hg-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2

; US-09-968-362A-22

Query Match 97.1%; Score 570; DB 4; Length 447;
Best Local Similarity 97.3%; Pred. No. 3.9e-59;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60	
Db	231	APEVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290	
Qy	61	PREEQYNSTYRVYSVLTVLDHQLWLNKGEYKCKVSNKGLPSSIEKTIKAK 110	
Db	291	PREEQYNSTYRVYSVLTVLDHQLWLNKGEYKCKVSNKGLPSSIEKTIKAK 340	

RESULT 2

US-09-485-737B-67

; Sequence 67, Application US/09485737B

; Patent No. 6350860

; GENERAL INFORMATION:

; APPLICANT: Buysee, Marie-Ange

; APPLICANT: Sablon, Erwin

; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

; FILE REFERENCE: INNS.015

; CURRENT APPLICATION NUMBER: US/09/485.737B

; CURRENT FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: PCT/EP 98/05165

```

; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match          95.7%; Score 562; DB 3; Length 468;
Best Local Similarity 95.5%; Pred. No. 3.7e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 311 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 360

RESULT 3
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

Query Match          95.7%; Score 562; DB 4; Length 468;
Best Local Similarity 95.5%; Pred. No. 3.7e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 311 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 360

RESULT 4
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```

US-09-499-846-12
; Sequence 12, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-12

Query Match          95.7%; Score 562; DB 4; Length 488;
Best Local Similarity 95.5%; Pred. No. 3.9e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 272 APELEGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 332 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 381

RESULT 5
US-09-499-846-10
; Sequence 10, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-10

Query Match          95.7%; Score 562; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 4e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 281 APELEGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 341 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 390

RESULT 6
US-09-499-846-8
; Sequence 8, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
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; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-8

Query Match          95.7%; Score 562; DB 4; Length 525;
Best Local Similarity 95.5%; Pred. No. 4.3e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 309 APELGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368
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Qy 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 110
Db 369 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 418
||:|||||

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match          95.7%; Score 562; DB 3; Length 711;
Best Local Similarity 95.5%; Pred. No. 6.5e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
||:|||||
Qy 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 110
Db 311 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 360
||:|||||

RESULT 8
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
```

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; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match          95.7%; Score 562; DB 4; Length 711;
Best Local Similarity 95.5%; Pred. No. 6.5e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
||:|||||
Qy 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 110
Db 311 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 360
||:|||||

RESULT 9
US-09-968-362A-20
; Sequence 20, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vPc gamma4 with a 30-amino acid leader peptide (Figure 2
; OTHER INFORMATION: B)
US-09-968-362A-20

Query Match          95.1%; Score 558; DB 4; Length 449;
Best Local Similarity 95.5%; Pred. No. 1e-57;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 233 APEFAGGSPVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
||:|||||
Qy 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 110
Db 293 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 342
||:|||||

RESULT 10
US-09-746-359A-62
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```

; Sequence 62, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-62

Query Match          95.1%; Score 558; DB 4; Length 559;
Best Local Similarity 95.5%; Pred. No. 1.4e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db      343 APEAGAPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 402
      |||

QY      61 PREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKSAK 110
      |||
Db      403 PREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKSAK 452
      |||

RESULT 11
US-09-746-359A-23
; Sequence 23, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match          95.1%; Score 558; DB 4; Length 594;
Best Local Similarity 95.5%; Pred. No. 1.4e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db      343 APEAGAPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 402
      |||

QY      61 PREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKSAK 110
      |||
Db      403 PREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKSAK 452
      |||

RESULT 12
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-21

Query Match          94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110

RESULT 13

US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Frigen, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

US-08-232-246A-21

Query Match 94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 110

RESULT 14

US-08-232-539D-55
; Sequence 55, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-232-539D-55

Query Match 94.9%; Score 557; DB 2; Length 116;
Best Local Similarity 94.5%; Pred. No. 2.2e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 6 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 66 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 115

RESULT 15

US-08-430-633-4
; Sequence 4, Application US/08430633
; Patent No. 5726286
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus B2LP2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 6 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 66 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 115

ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,633
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: I9G1 Fc
US-08-430-633-4

Query Match 94.9%; Score 557; DB 1; Length 212;
Best Local Similarity 94.5%; Pred. No. 5e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
||:|||||
Db 14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
Qy 61 PREEQYNSTYRVWSVLTVLHODWLNKGKEYCKVSNKGLPSSIETISKAK 110
|||:|||||
Db 74 PREEQYNSTYRVWSVLTVLHODWLNKGKEYCKVSNKGLPAPIETISKAK 123

Search completed: November 17, 2005, 07:13:22
Job time : 25.6119 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 84.3836 Seconds
(without alignments)
545.427 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLPPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubaa/US09D_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09E_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	98.6	110	18	US-10-959-318-9
2	579	98.6	110	18	US-10-959-318-10
3	570.5	97.2	329	20	US-11-102-403-25
4	570	97.1	435	10	US-09-932-812-22
5	570	97.1	435	16	US-10-761-593A-22
6	570	97.1	435	20	US-11-016-518A-22
7	570	97.1	435	20	US-11-017-185-22
8	570	97.1	447	10	US-09-968-362-22
9	570	97.1	447	16	US-10-800-497-22
10	570	97.1	447	16	US-10-800-449-22
11	565	96.3	110	18	US-10-959-318-13
					Sequence 9, Appli
					Sequence 10, Appl
					Sequence 25, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 13, Appl

12	565	96.3	110	18	US-10-959-318-14	Sequence 14, Appl
13	563	95.9	110	18	US-10-959-318-7	Sequence 7, Appli
14	563	95.9	110	18	US-10-959-318-8	Sequence 8, Appli
15	562.5	95.8	109	18	US-10-959-318-11	Sequence 11, Appl
16	562.5	95.8	109	18	US-10-959-318-12	Sequence 12, Appl
17	562	95.7	468	14	US-10-071-485-67	Sequence 67, Appl
18	562	95.7	468	18	US-10-985-581-67	Sequence 67, Appl
19	562	95.7	488	15	US-10-683-255-12	Sequence 12, Appl
20	562	95.7	497	15	US-10-683-255-10	Sequence 10, Appl
21	562	95.7	500	18	US-10-627-556-274	Sequence 274, App
22	562	95.7	500	18	US-10-627-556-276	Sequence 276, App
23	562	95.7	525	15	US-10-683-255-8	Sequence 8, Appli
24	562	95.7	711	14	US-10-071-485-90	Sequence 90, Appl
25	562	95.7	711	18	US-10-985-581-90	Sequence 90, Appl
26	561	95.6	110	20	US-11-018-102-23	Sequence 23, Appl
27	561	95.6	330	17	US-10-706-689-3	Sequence 3, Appli
28	561	95.6	330	18	US-10-988-360-3	Sequence 3, Appli
29	561	95.6	330	20	US-11-102-403-26	Sequence 26, Appl
30	561	95.6	447	15	US-10-474-832-6	Sequence 6, Appli
31	560	95.4	227	17	US-10-822-231-124	Sequence 124, App
32	560	95.4	227	17	US-10-822-231-281	Sequence 281, App
33	559	95.2	110	20	US-11-018-102-25	Sequence 25, Appl
34	559	95.2	227	17	US-10-822-231-123	Sequence 123, App
35	559	95.2	227	17	US-10-822-231-127	Sequence 127, App
36	558	95.1	109	18	US-10-627-556-270	Sequence 270, App
37	558	95.1	216	18	US-10-627-556-272	Sequence 272, App
38	558	95.1	227	17	US-10-822-231-130	Sequence 130, App
39	558	95.1	227	17	US-10-822-231-134	Sequence 134, App
40	558	95.1	227	17	US-10-822-231-296	Sequence 296, App
41	558	95.1	232	14	US-10-008-063-28	Sequence 28, Appl
42	558	95.1	232	14	US-10-008-063-32	Sequence 32, Appl
43	558	95.1	250	14	US-10-152-363A-35	Sequence 35, Appl
44	558	95.1	251	14	US-10-152-363A-31	Sequence 31, Appl
45	558	95.1	251	14	US-10-152-363A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)
US-10-959-318-9

Query Match 98.6%; Score 579; DB 18; Length 110;
Best Local Similarity 95.1%; Pred. No. 1.1e-48;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

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Qy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110

RESULT 2
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and e (E269)
US-10-959-318-10

Query Match 98.6%; Score 579; DB 18; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.1e-48;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Qy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110

RESULT 3
US-11-102-403-25
; Sequence 25, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PABREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STUBENRAUCH, PAMELA
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUUT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 329
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-102-403-25

Query Match 97.2%; Score 570.5; DB 20; Length 329;
Best Local Similarity 99.1%; Pred. No. 2.5e-47;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db 114 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 172

Qy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 173 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 222

RESULT 4
US-09-932-812-22
; Sequence 22, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human erythropoietin with increased biological activity
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C)
US-09-932-812-22

Query Match 97.1%; Score 570; DB 10; Length 435;
Best Local Similarity 97.3%; Pred. No. 3.8e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db 219 APEVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278

Qy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 279 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 328

RESULT 5
US-10-761-593A-22
; Sequence 22, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human erythropoietin with high biological activity
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2)
US-10-761-593A-22

Query Match 97.1%; Score 570; DB 16; Length 435;
Best Local Similarity 97.3%; Pred. No. 3.8e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 219 APEVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278
Qy 61 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 279 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPASIEKTIISKAK 328

RESULT 6

US-11-016-518A-22
Sequence 22, Application US/11016518A
Publication No. US20050124045A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
TITLE OF INVENTION: Biological activities
FILE REFERENCE: 02SUN2004D1
CURRENT APPLICATION NUMBER: US/11/016,518A
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 435
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2)
US-11-016-518A-22

Query Match 97.1%; Score 570; DB 20; Length 435;
Best Local Similarity 97.3%; Pred. No. 3.8e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 219 APEVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278
Qy 61 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 279 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPASIEKTIISKAK 328

RESULT 7

US-11-017-185-22
Sequence 22, Application US/11017185
Publication No. US20050142642A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological
TITLE OF INVENTION: activities
FILE REFERENCE: 02SUN2001D2
CURRENT APPLICATION NUMBER: US/11/017,185
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1

SEQ ID NO 22
LENGTH: 435
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2)
US-11-017-185-22

Query Match 97.1%; Score 570; DB 20; Length 435;
Best Local Similarity 97.3%; Pred. No. 3.8e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 219 APEVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278
Qy 61 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 279 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPASIEKTIISKAK 328

RESULT 8

US-09-968-362-22
Sequence 22, Application US/09968362
Publication No. US20030082679A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
TITLE OF INVENTION: Biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/09/968,362
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 447
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2)
US-09-968-362-22

Query Match 97.1%; Score 570; DB 10; Length 447;
Best Local Similarity 97.3%; Pred. No. 3.9e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 231 APEVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290
Qy 61 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 291 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPASIEKTIISKAK 340

RESULT 9

US-10-800-497-22
Sequence 22, Application US/10800497
Publication No. US20040259209A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
TITLE OF INVENTION: stimulating factor with
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/10/800,497
CURRENT FILING DATE: 2004-03-15

```

; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide
; OTHER INFORMATION: (Figure 2
; OTHER INFORMATION: C)
US-10-800-497-22

Query Match          97.1%; Score 570; DB 16; Length 447;
Best Local Similarity 97.3%; Pred. No. 3.9e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 231 APEVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 340

RESULT 10
US-10-800-449-22
; Sequence 22, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
; FILE REFERENCE: increased biological activities
; TITLE OF INVENTION: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2
; OTHER INFORMATION: C)
US-10-800-449-22

Query Match          97.1%; Score 570; DB 16; Length 447;
Best Local Similarity 97.3%; Pred. No. 3.9e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 231 APEVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 340

RESULT 11
US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R

```

```

; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-13

Query Match          96.3%; Score 565; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 2.4e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSEDEPEVKFNWYVDGVEVHNAKTK 60

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 110

RESULT 12
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-14

Query Match          96.3%; Score 565; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 2.4e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVAGGSPVFLPPPKPDKDTLMISRTPEVTCVVVDVSEDEPEVKFNWYVDGVEVHNAKTK 60

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 110

RESULT 13
US-10-959-318-7

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; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
; OTHER INFORMATION: mutations
US-10-959-318-7

Query Match 95.9%; Score 563; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 3.8e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
| : |||||
Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVKFNWYVDGVEVHNAKTK 60
| : |||||

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
| : |||||
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
| : |||||

RESULT 14
US-10-959-318-8
; Sequence 8, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-8

Query Match 95.9%; Score 563; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 3.8e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
| : |||||
Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
| : |||||

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
| : |||||

Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
| : |||||

RESULT 15
US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-11

Query Match 95.8%; Score 562.5; DB 18; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.2e-47;
Matches 108; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
| : |||||
Db 1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVKFNWYVDGVEVHNAKTK 59
| : |||||

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
| : |||||
Db 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
| : |||||

Search completed: November 17, 2005, 07:37:36
Job time : 85.3836 secs

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.9087 Seconds
(without alignments)
473.187 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APVAGGSRVFLPPKPKDT.....CKVSNKGLPSSIEKTIKRAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	98.1	110	3 AAY54998	Mutated C
2	570.5	97.2	109	3 AAY54996	Mutated C
3	557	94.9	110	3 AAR27680	Human imm
4	557	94.9	110	2 AAR41684	Human IGG
5	557	94.9	110	8 ADH75385	Human IGG
6	553	94.2	109	7 ADP25659	Binding d
7	553	94.2	110	2 AAR41717	Undefined
8	552	94.0	109	5 AAE28089	Human imm
9	552	94.0	110	8 ADH75415	CH2 regio
10	551	93.9	110	8 ADL90103	Human imm
11	550	93.7	110	8 ADH75413	CH2 regio
12	549	93.5	109	2 AAR67438	OKT3 mono
13	545	92.8	109	7 ADP25761	Binding d
14	543.5	92.6	109	2 AAR41709	Undefined
15	543.5	92.6	109	3 AAY54997	Mutated C
16	541	92.2	105	2 AAY42626	Human IGG
17	533	90.8	110	2 AAR41713	Undefined
18	528	89.9	102	8 ADJ52129	CH1 delet
19	526	89.6	102	8 ADJ52132	CH1 delet
20	415	70.7	110	2 AAW71023	Mus muscu
21	397	67.6	110	1 AAR83207	Sequence
22	357	60.8	72	8 ADL15711	Human imm
23	344	58.6	66	2 AAR75349	C-gamma-1
24	344	58.6	66	2 AAR75351	C-gamma-1
25	318	54.2	76	8 ADL15713	Human imm

26	286	48.7	56	1 AAR83204	Sequence
27	281	47.9	56	1 AAR83201	Sequence
28	281	47.9	56	1 AAR83203	Sequence
29	280	47.7	56	1 AAR83202	Sequence
30	275	46.8	56	1 AAR83206	Sequence
31	275	46.8	56	1 AAR83205	Sequence
32	249	42.4	46	8 ADR59138	Human IGG
33	234	39.9	46	8 ADR59139	Human IGG
34	232.5	39.6	110	2 AAR33315	Variant I
35	221	37.6	46	8 ADR59142	Rhesus mo
36	215	36.6	46	8 ADR59143	Rhesus mo
37	209	35.6	46	8 ADR59140	Rhesus mo
38	209	35.6	46	8 ADR59141	Crab-eati
39	203.5	34.7	110	2 AAR33314	Variant I
40	201.5	34.3	110	2 AAR33316	Variant I
41	199	33.9	96	3 AAB53640	Human col
42	198	33.7	46	8 ADR59148	Camel IGG
43	194	33.0	46	8 ADR59145	Pig IGG2a
44	193.5	33.0	110	2 AAR33693	Variant I
45	192	32.7	46	8 ADR59147	Llama IGG

ALIGNMENTS

RESULT 1

AAY54998

ID AAY54998 standard; protein; 110 AA.

XX

AC AAY54998;

XX

DT 17-FEB-2000 (first entry)

XX

DE Mutated CH2 sequence G1deltaaac.

XX

KW Binding molecule: CH2 sequence; complement dependent lysis; FcgammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; IGG heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
 KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; Goodpasture disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.

XX Synthetic.

OS

PN WO9558572-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001441.

XX

PR 08-MAY-1998; 98GB-00009951.

XX

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX

XX Armour KL, Clark MR, Williamson LM;

XX WPI; 2000-039075/03.

XX

PT Immunoglobulin-derived binding molecules that do not activate complement
 or trigger cytotoxic activities and maintaining desirable immunoglobulin
 properties.

XX Claim 12; Fig 17; 81pp; English.

XX

CC This sequence represents the mutated CH2 molecule G1deltaaac, and is a
 binding molecule of the invention. The recombinant binding molecule is
 capable of binding a target molecule without triggering complement
 dependent lysis, or the cell-mediated destruction of the target
 comprises: (a) a binding domain capable of binding a target molecule; and
 (b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially Fc gammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of graft-vs-
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through Fc gammaR and desirable
 CC Igg properties have been retained. The polypeptides do not contain non-
 CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)
 XX
 CC Sequence 110 AA;

Query Match 98.1%; Score 576; DB 3; Length 110;
 Best Local Similarity 99.1%; Pred. No. 1.4e-51;
 Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 QY 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 110
 DB 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 110

RESULT 2
 ID AAY54996 standard; protein; 109 AA.
 XX AAY54996;
 XX 17-FEB-2000 (first entry)
 XX Mutated CH2 sequence Gdeltaaab.
 KW Binding molecule; CH2 sequence; complement dependent lysis; Fc gammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; Igg heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
 KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.
 XX Synthetic.
 XX WO9958572-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-CB001441.
 XX 08-MAY-1998; 98GB-00009951.
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX Armour KL, Clark MR, Williamson LM;
 XX WPI; 2000-039075/03.
 XX Immunoglobulin-derived binding molecules that do not activate complement
 PT or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.
 XX Claim 12; Fig 17; 81pp; English.
 PS This sequence represents the mutated CH2 molecule Gdeltaaab, and is a
 CC binding molecule of the invention. The recombinant binding molecule is
 CC capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially Fc gammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of graft-vs-
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through Fc gammaR and desirable
 CC Igg properties have been retained. The polypeptides do not contain non-
 CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)
 XX
 CC Sequence 109 AA;

Query Match 97.2%; Score 570.5; DB 3; Length 109;
 Best Local Similarity 99.1%; Pred. No. 5.3e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
 QY 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 110
 DB 60 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 109

RESULT 3
 AAR27680
 ID AAR27680 standard; protein; 110 AA.
 XX AAR27680;
 XX 25-MAR-2003 (revised)
 DT 10-MAR-1993 (first entry)
 XX Human immunoglobulin IgG1 CH2 region.
 XX Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab.
 XX Homo sapiens.
 XX WO9216562-A1.
 XX 01-OCT-1992.
 XX 12-MAR-1992; 92WO-GB000445.
 XX 12-MAR-1991; 91GB-00005245.
 XX (LYNX-) LYNXVALE LTD.
 XX Clark MR;
 XX WPI; 1992-349162/42.

XX Humanised antibodies having modified allotypic determinant - useful for
PT matching allotypes in therapy with decreased likelihood of causing
PT undesirable immune responses.
XX
XX
PS Disclosure; Fig 4c; 57pp; English.
XX
XX In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.
CC The inventor's propose eliminating these allotypes by amino acid changes
CC to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype
CC sites (1, 2 and 17) are located within the CH2 domain. New "isotypes"
CC should be suitable for therapeutic use in all patients. See AAR27678-
CC R27681. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 110 AA;

Query Match 94.9%; Score 557; DB 2; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.3e-49;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVHLQDWLNCKEYKCKVSNKGLPSSIEKTTISKAK 110
|| : |||||
Db 61 PREEQYNSTYRVVSVLTVHLQDWLNCKEYKCKVSNKGLPAPIEKTTISKAK 110
|| : |||||

RESULT 4
AAR41684
ID AAR41684 standard; protein; 110 AA.
XX
XX AAR41684;
XX
XX 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
XX Undefined ORF2 encoded by pAH4602.
DE
XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;
KW chain; variable; constant; region; anti-human; transferrin; receptor;
KW antibody; brain; capillary; endothelial cell; conjugate;
KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy;
KW Parkinsons disease; Alzheimers disease.
XX
XX Synthetic.
OS
XX WO9310819-A1.
PN
XX 10-JUN-1993.
PD
XX 24-NOV-1992; 92WO-US010206.
PF
XX 26-NOV-1991; 91US-00800458.
PR
XX (ALKE-) ALKERMES INC.
PA
XX Friden PM;
PI
XX WPI; 1993-196742/24.
DR
XX N-PSDB; AAQ43844.
DR
XX
XX Antibody conjugates specific for transferrin receptor - used for
PT diagnosis and treatment of cancer, AIDS and neurological disorders.
PT
XX Disclosure; Fig 11K; 151pp; English.
PS
XX The sequences given in AAR41682-85 are encoded by the expression vector,
CC pAH4602. This vector contains open reading frames encoding the heavy
CC chain variable region (VH) of the antibody 128.1, an ampicillin
CC resistance gene and a histidine (histidinol) selection marker.
CC
XX Transcription of the VH gene is from the VH promoter of the murine 27.44

CC gene. The vector also includes a heavy chain immunoglobulin enhancer and
CC the human gamma constant region (CH). The VH region of 128.1 was
CC isolated by polymerase chain reaction and cloned into plasmid pAH4274.
CC This was achieved by digesting the plasmid and the product with EcoRV and
CC NheI. The VH gene was inserted in-frame with the human gamma CH region
CC CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an
CC anti-human transferrin receptor antibody which binds to the transferrin
CC receptor on brain capillary endothelial cells. This antibody may be used
CC in a conjugate in which it is linked to a neuro- pharmaceutical or
CC diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 110 AA;

Query Match 94.9%; Score 557; DB 2; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.3e-49;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVHLQDWLNCKEYKCKVSNKGLPSSIEKTTISKAK 110
|| : |||||
Db 61 PREEQYNSTYRVVSVLTVHLQDWLNCKEYKCKVSNKGLPAPIEKTTISKAK 110
|| : |||||

RESULT 5
ADH75385
ID ADH75385 standard; protein; 110 AA.
XX
XX ADH75385;
XX
XX 22-APR-2004 (first entry)
DT
XX Human IgG1 CH2 region.
DE
XX
XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
KW autoimmune disease; human; IgG; immunoglobulin.
XX
XX Homo sapiens.
OS
XX US2004002587-A1.
PN
XX 01-JAN-2004.
PD
XX 20-FEB-2003; 2003US-00370749.
PF
XX 20-FEB-2002; 2002US-0358161P.
PR
XX (WATK/) WATKINS J D.
PA (ALLA/) ALLAN B.
XX
XX Watkins JD, Allan B;
PI
XX WPI; 2004-070755/07.
DR
XX
XX New composition comprising a variant of a parent polypeptide having at
PT least a portion of a Fe region, useful in treating e.g., autoimmune
PT diseases.
XX
PS Claim 20; SEQ ID NO 23; 62pp; English.
XX
XX The invention relates to a new composition comprises a variant of a
CC parent polypeptide having at least a portion of a Fe region. The variant
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
CC presence of effector cells more effectively than the parent polypeptide
CC and comprises at least one amino acid modification at position 280 in the
CC Fc region. The composition is useful in treating diseases e.g.,
CC autoimmune diseases. The present sequence represents the amino acid
CC sequence of a human immunoglobulin G, IgG, CH region.

```
XX SQ Sequence 110 AA;
Query Match 94.9%; Score 557; DB 8; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.3e-49;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELGGPSVFLFPPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

OY 61 PREEQYNSTYRVVSVLTVHLQDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQYNSTYRVVSVLTVHLQDMLNGKEYCKVSNKALPAPIEKTIISKAK 110

RESULT 6
ADD25659
ID ADD25659 standard; protein; 109 AA.
XX AC ADD25659;
XX DT 15-JAN-2004 (first entry)
XX DE Binding domain-immunoglobulin fusion protein-associated protein #107.
XX KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type 1 diabetes mellitus; multiple sclerosis; autoimmune disease.
XX OS Unidentified.
XX PN US2003118592-A1.
XX PD 26-JUN-2003.
XX PF 25-JUL-2002; 2002US-00207655.
XX PR 17-JAN-2001; 2001US-0367358P.
XX PR 17-JAN-2002; 2002US-00053530.
XX PR 03-JUN-2002; 2002US-0385691P.
XX PA (GENE-) GENE-CRAFT INC.
XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WI; 2003-801317/75.
XX PT New binding domain-immunoglobulin fusion protein, useful for treating a
XX PT subject having or suspected of having a malignant condition or a B-cell
XX PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX PS Disclosure; SEQ ID NO 220; 157pp; English.
XX CC The invention relates to a binding domain-immunoglobulin fusion protein
XX CC comprising a binding domain polypeptide that is fused to an
XX CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CC CH2 constant region polypeptide that is fused to the hinge region
XX CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX CC polypeptide that is fused to the CH2 constant region polypeptide. The
XX CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
XX CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
XX CC region polypeptide, derived from (a) having 3 or more cysteine residues;
XX CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
XX CC contains 2 cysteine residues, where the first cysteine is not mutated; a
XX CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
XX CC (a) having 3 or more cysteine residues, where the mutated human IgG1
XX CC immunoglobulin hinge region polypeptide contains no more than one
```

```
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type 1 diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX SQ Sequence 109 AA;
Query Match 94.2%; Score 553; DB 7; Length 109;
Best Local Similarity 94.5%; Pred. No. 3.4e-49;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 PPVAGGSPVFLFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 1 PELGGPSVFLFPPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

OY 62 REEQYNSTYRVVSVLTVHLQDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQYNSTYRVVSVLTVHLQDMLNGKEYCKVSNKALPAPIEKTIISKAK 109

RESULT 7
AAR41717
ID AAR41717 standard; protein; 110 AA.
XX AC AAR41717;
XX DT 25-MAR-2003 (revised)
XX DT 20-OCT-1993 (first entry)
XX DE Undefined ORF2 encoded by plasmid pAH4808.
XX KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
XX KW light; chain; variable; constant; region; anti-human; pAH4807;
XX KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
XX KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
XX KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
XX KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX OS Synthetic.
XX PN WO9310819-A1.
XX PD 10-JUN-1993.
XX PF 24-NOV-1992; 92WO-US010206.
XX PR 26-NOV-1991; 91US-00800458.
XX PA (ALKE-) ALKERMES INC.
XX PI Friden PM;
```

XX WPI; 1993-196742/24.
 DR N-PSDB; AAQ43848.
 XX
 PT Antibody conjugates specific for transferrin receptor - used for
 XX diagnosis and treatment of cancer, AIDS and neurological disorders.
 XX
 PS Disclosure; Fig 19J; 151pp; English.
 XX
 CC The sequences given in AAR41715-18 are encoded by the expression vector
 CC pAH4808. This vector represents the cloning of the human gamma isotype,
 CC gamma-4, with the variable region of the murine monoclonal antibody
 CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the
 CC heavy chain (VH) is derived from a murine source and the sequences
 CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,
 CC in combination with the chimeric light chain vector, pAG4611 (see also
 CC AAQ43845), was transfected into SP2/0 cells and clones were isolated.
 CC 128.1 is an anti-human transferrin receptor antibody which binds to the
 CC transferrin receptor on brain capillary endothelial cells. This antibody
 CC may be used in a conjugate in which it is linked to a neuropharmaceutical
 CC or diagnostic agent. The conjugate may be used to treat or prevent
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 110 AA;
 SQ
 Query Match 94.2%; Score 553; DB 2; Length 110;
 Best Local Similarity 94.5%; Pred. No. 3.4e-49;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 1 APEFLGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 QY 61 PREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 DB 61 PREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 RESULT 8
 AAE28089
 ID AAE28089 standard; protein; 109 AA.
 AC AAE28089;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.
 XX
 KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
 KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
 KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
 KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
 KW virucide.
 XX
 OS Homo sapiens.
 XX
 PN WO200260919-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 12-DEC-2001; 2001WO-US048432.
 XX
 PR 12-DEC-2000; 2000US-0254884P.
 XX
 PR 09-MAY-2001; 2001US-0289760P.
 XX
 XX (MEDI-) MEDIMUNE INC.
 PA
 XX Dall'acqua W, Johnson LS, Ward BS;
 XX
 XX WPI; 2002-666925/71.
 XX

PT Modified immunoglobulins useful in the treatment of autoimmune diseases,
 PT comprises at least one amino acid modification relative to a wild-type
 PT immunoglobulin constant domain.
 XX
 XX Disclosure; Page 138; 147pp; English.
 XX
 CC The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an Fc constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 CC vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 94.0%; Score 552; DB 5; Length 109;
 Best Local Similarity 94.5%; Pred. No. 4.3e-49;
 Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 1 APELLGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 QY 61 PREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKA 109
 DB 61 PREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAIEKTSKA 109
 RESULT 9
 ADH75415
 ID ADH75415 standard; protein; 110 AA.
 XX
 AC ADH75415;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE CH2 region K290S variant.
 XX
 KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
 KW autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN US2004002587-A1.
 XX
 PD 01-JAN-2004.
 XX
 PF 20-FEB-2003; 2003US-00370749.
 XX
 PR 20-FEB-2002; 2002US-0358161P.
 XX
 XX (WATK/) WATKINS J D.
 PA (ALLA/) ALLAN B.
 XX
 PI Watkins JD, Allan B;
 XX
 DR WPI; 2004-070755/07.
 XX
 PT New composition comprising a variant of a parent polypeptide having at
 PT least a portion of a Fc region, useful in treating e.g., autoimmune
 PT diseases.
 XX
 XX Disclosure; SEQ ID NO 53; 62pp; English.
 XX
 CC The invention relates to a new composition comprises a variant of a
 CC parent polypeptide having at least a portion of a Fc region. The variant
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
 CC presence of effector cells more effectively than the parent polypeptide
 CC and comprises at least one amino acid modification at position 280 in the
 CC Fc region. The composition is useful in treating diseases e.g.,

CC autoimmune diseases. The present sequence represents a CH2 region
CC variant.
SQ Sequence 110 AA;

Query Match 94.0%; Score 552; DB 8; Length 110;
Best Local Similarity 93.6%; Pred. No. 4.4e-49;
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
||:|||||||||||||||||||||||||||||||||||||||||
Db 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTS 60
||:|||||||||||||||||||||||||||||||||||||||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
||:|||||||||||||||||||||||||||||||||||||||||
Db 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKALPAPIEKTIISKAK 110
||:|||||||||||||||||||||||||||||||||||||||||

RESULT 10
ADL90103
ID ADL90103 standard; protein; 110 AA.
XX AC ADL90103;
XX 17-JUN-2004 (first entry)
XX Human immunoglobulin CH2 region, SEQ ID 2.
XX Immune response; immunoglobulin; Ig; CH2 region; human.
XX Homo sapiens.
XX WO2004027049-A2.
XX 01-APR-2004.
XX 18-SEP-2003; 2003WO-US030188.
XX 20-SEP-2002; 2002US-0412219P.
XX 14-MAR-2003; 2003WO-US007995.
XX (ASTR-) ASTRAL INC.
XX Bot A, Wang L, Smith D, Phillips B;
XX WPI; 2004-295415/27.
XX Generating an immune response to an antigen, useful for generating
PT desired T cell responses comprises administering an immunoglobulin having
PT one peptide epitope of the antigen attached to the immunoglobulin.
XX Disclosure; Page 11; 154pp; English.

The present invention relates to a method for generating an immune
CC response to an antigen in a patient. The method comprises administering
CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
CC least one peptide epitope of the antigen attached to the Ig or its
CC portion and administering the immunoglobulin or its portion in
CC conjunction with a RNA segment. A recombinant human Ig molecule capable
CC of binding to an Fc gamma receptor (FcgammaR) of an antigen presenting
CC cell (APC) was used to illustrate the invention. The recombinant human Ig
CC molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a
CC hinge region (ADL90104) and a flanking peptide (ADL90105).

SQ Sequence 110 AA;

Query Match 93.9%; Score 551; DB 8; Length 110;
Best Local Similarity 93.6%; Pred. No. 5.5e-49;
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
||:|||||||||||||||||||||||||||||||||||||||||
Db 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
||:|||||||||||||||||||||||||||||||||||||||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
||:|||||||||||||||||||||||||||||||||||||||||
Db 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVFNKALPAPIEKTIISKAK 110
||:|||||||||||||||||||||||||||||||||||||||||

RESULT 11
ADH75413
ID ADH75413 standard; protein; 110 AA.
XX AC ADH75413;
XX 22-APR-2004 (first entry)
XX CH2 region D280H variant.
XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
KW autoimmune disease.
XX Unidentified.
XX US2004002587-A1.
XX 01-JAN-2004.
XX 20-FEB-2003; 2003US-00370749.
XX 20-FEB-2002; 2002US-0358161P.
XX (WATK/) WATKINS J D.
XX (ALLA/) ALLAN B.
XX Watkins JD, Allan B;
XX WPI; 2004-070755/07.
XX New composition comprising a variant of a parent polypeptide having at
PT least a portion of a Fe region, useful in treating e.g., autoimmune
PT diseases.
XX Disclosure; SEQ ID NO 51; 62pp; English.

The invention relates to a new composition comprises a variant of a
CC parent polypeptide having at least a portion of a Fc region. The variant
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
CC presence of effector cells more effectively than the parent polypeptide
CC and comprises at least one amino acid modification at position 280 in the
CC Fc region. The composition is useful in treating diseases e.g.,
CC autoimmune diseases. The present sequence represents a CH2 region
CC variant.

SQ Sequence 110 AA;

Query Match 93.7%; Score 550; DB 8; Length 110;
Best Local Similarity 93.6%; Pred. No. 7e-49;
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
||:|||||||||||||||||||||||||||||||||||||||||
Db 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
||:|||||||||||||||||||||||||||||||||||||||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
||:|||||||||||||||||||||||||||||||||||||||||
Db 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKALPAPIEKTIISKAK 110
||:|||||||||||||||||||||||||||||||||||||||||

RESULT 12
AAR67438
ID AAR67438 standard; protein; 109 AA.
XX AC AAR67438;
XX 25-MAR-2003 (revised)

DT 08-JUL-1995 (first entry)
 XX OKT3 monoclonal antibody fragment.
 XX
 KW OKT3; monoclonal antibody; antibody engineering; immunosuppressive;
 KW humanized antibody.
 XX
 OS Mus musculus.
 XX
 PN W09428027-A1.
 XX
 XX 08-DEC-1994.
 XX
 XX 01-JUN-1994; 94WO-US006198.
 XX
 XX 01-JUN-1993; 93US-00070116.
 XX
 XX (ARCH-) ARCH DEV CORP.
 XX
 XX Bluestone JA, Zivin RA, Jolliffe L;
 PI
 XX WPI; 1995-022721/03.
 DR P-PSDB; AAQ75356.
 XX
 XX New humanised OKT3 antibody with mutated Fc receptor binding region -
 PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
 PT cell activating side effects of wild type antibody.
 XX
 XX Disclosure; Page 82-87; 135pp; English.
 XX
 XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-
 CC cell activating and immunosuppressive activity, and is used to treat
 CC transplant patients to prevent rejection. The antibody can be engineered
 CC to contain a human Fc region. By transferring the binding specificity
 CC into a human framework, the immunogenicity is reduced without affecting
 CC the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 93.5%; Score 549; DB 2; Length 109;
 Best Local Similarity 94.5%; Pred. No. 8.8e-49;
 Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PPVAGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKP 61
 DB 1 PELLGGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKP 60
 QY 62 REEQYNSTRVRSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 DB 61 REEQFNSTRVRSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
 RESULT 13
 ID ADD25761 standard; protein; 109 AA.
 XX
 AC ADD25761;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 XX Binding domain-immunoglobulin fusion protein-associated protein #149.
 DE
 XX Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antithyroid; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.

XX US2003118592-A1.
 XX
 XX 26-JUN-2003.
 XX
 XX 25-JUL-2002; 2002US-00207655.
 XX
 XX 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 XX (GENE-) GENE-CRAFT INC.
 XX
 XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 PI WPI; 2003-801317/75.
 XX
 XX New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 XX Disclosure; SEQ ID NO 322; 157pp; English.
 XX
 XX The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docId=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 92.8%; Score 545; DB 7; Length 109;
 Best Local Similarity 93.6%; Pred. No. 2.3e-48;
 Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 2 PPVAGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKP 61
 DB 1 PELLGGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKP 60

```

QY      62 REEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110
Db      61 REEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPAPIEKTISKAK 109

RESULT 14
AAR41709
ID      AAR41709 standard; protein; 109 AA.
XX
AC      AAR41709;
XX
DT      25-MAR-2003 (revised)
DT      20-OCT-1993 (first entry)
XX
DE      Undefined ORF2 encoded by plasmid pAH4625.
XX
KW      Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW      light; chain; variable; constant; region; anti-human; pAH4807;
KW      transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW      endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW      diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW      Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
OS      Synthetic.
XX
PN      WO9310819-A1.
XX
PD      10-JUN-1993.
XX
PF      24-NOV-1992; 92WO-US010206.
XX
PR      26-NOV-1991; 91US-00800458.
XX
PA      (ALKE-) ALKERMES INC.
XX
PI      Friden PM;
XX
WPI; 1993-196742/24.
DR      N-PSDB; AAQ43846.
XX
PT      Antibody conjugates specific for transferrin receptor - used for
PT      diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
PS      Disclosure; Fig 17J; 151pp; English.
XX
CC      The sequences given in AAR41707-09 are encoded by the expression vector
CC      pAH4625. This vector represents the cloning of the human gamma isotype,
CC      gamma-2, with the variable region of the murine monoclonal antibody
CC      128.1. This plasmid encodes a chimeric monoclonal antibody in which the
CC      heavy chain (VH) is derived from a murine source and the sequences
CC      encoding CH1, CH2 and CH3 are derived from a human source. This vector,
CC      in combination with the chimeric light chain vector, pAG4611 (see also
CC      AAQ43845), was transfected into SP2/0 cells and clones were isolated.
CC      128.1 is an anti-human transferrin receptor antibody which binds to the
CC      transferrin receptor on brain capillary endothelial cells. This antibody
CC      may be used in a conjugate in which it is linked to a neuropharmaceutical
CC      or diagnostic agent. The conjugate may be used to treat or prevent
CC      neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC      Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC      methods. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 109 AA;

Query Match          92.6%; Score 543.5; DB 2; Length 109;
Best Local Similarity 92.7%; Pred. No. 3.3e-48;
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY      1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKATK 60
Db      1 APPVA-GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKATK 59

QY      61 PREEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110

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```

Db      60 PREEQNSTYRVSVLTVHODWLNKGKCKVSNKGLPAPIEKTISKTK 109

RESULT 15
AA54997
ID      AA54997 standard; protein; 109 AA.
XX
AC      AA54997;
XX
DT      17-FEB-2000 (first entry)
XX
DE      Mutated CH2 sequence G2deltaa.
XX
KW      Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW      cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW      B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW      Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW      bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW      alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW      autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW      neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
KW      sickle cell anaemia; coronary artery occlusion.
XX
OS      Synthetic.
XX
PN      WO9958572-A1.
XX
PD      18-NOV-1999.
XX
PF      07-MAY-1999; 99WO-GB001441.
XX
PR      08-MAY-1998; 98GB-00009951.
XX
PA      (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI      Armour KL, Clark MR, Williamson LM;
XX
WPI; 2000-039075/03.
XX
PT      Immunoglobulin-derived binding molecules that do not activate complement
PT      or trigger cytotoxic activities and maintaining desirable immunoglobulin
PT      properties.
XX
PS      Claim 12; Fig 17; 81pp; English.
XX
CC      This sequence represents the mutated CH2 molecule G2deltaa, and is a
CC      binding molecule of the invention. The recombinant binding molecule is
CC      capable of binding a target molecule without triggering complement
CC      dependent lysis, or the cell-mediated destruction of the target
CC      comprises: (a) a binding domain capable of binding a target molecule; and
CC      (b) an effector domain that is homologous to all or part of a constant
CC      domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC      molecule is used to bind a target molecule (especially FcgammaRIIb
CC      causing inhibition of B cell activation, mast cell degranulation or
CC      phagocytosis). The binding molecule can be used to prevent or inhibit the
CC      binding of a second binding molecule, e.g. an antibody, to the target
CC      molecule. The binding molecule is useful for the treatment of graft-vs-
CC      host disease, organ transplant rejection, bone-marrow transplant
CC      rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC      autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.
CC      foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
CC      chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC      (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC      coronary artery occlusion). The binding molecules do not activate
CC      complement or trigger cytotoxic activities through FcgammaRIIb and desirable
CC      IgG properties have been retained. The polypeptides do not contain non-
CC      human amino acids, and are therefore likely to have reduced
CC      immunogenicity. Further, they still bind Protein A, which is consistent
CC      with being able to cross the human placenta through interaction with FcRn
CC      (neonatal Fc receptor)
XX
SQ      Sequence 109 AA;

```

Query Match 92.6%; Score 543.5; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 3.3e-48;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
QY 1 APPVAGGSPVELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKNNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLFPKPFDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 60 PREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109

Search completed: November 17, 2005, 07:47:00
Job time : 89.9087 secs

11/17/05 11:27:19 AM

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C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C/Accession: B30554
R/Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A/Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A/Reference number: A30554; MUID:89093962; PMID:2492052
A/Accession: B30554
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-105 <FOL>
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/20-88/Domain: immunoglobulin homology <IMM>

Query Match      21.7%; Score 127.5; DB 2; Length 105;
Best Local Similarity 30.8%; Pred. No. 1.3e-05;
Matches 33; Conservative 21; Mismatches 44; Indels 7; Gaps 4

Qy      8 PSVLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPREEQY 66
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :
Db      6 PSVTLFPPSKEE--LDTKATVVCILSD--FYPGSVNVVWKADGSIINQNVKTTQASKQS 61
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :

Qy      67 NSTYRVVSVTLVHLQDWLNKGKEYCKYKSVNKGKLPSSIEKTIKAK 110
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :
Db      62 NSKYAASSYLTLTGSEWKSSTCYEVTHEG--STVTKTVKPSSE 103
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :

RESULT 8
B26434
Ig lambda-5 chain C region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C/Accession: B26434
R/Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A/Title: Lambda-5, a new light-chain-related locus selectively expressed in pro
A/Reference number: A26434; MUID:87065143; PMID:3024017
A/Accession: B26434
A/Molecule type: mRNA
A/Residues: 1-105 <SAK>
A/Cross-references: GB:M30387
A/Note: the authors translated the codon TAC for residue 84 as Thr
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match      21.6%; Score 126.5; DB 2; Length 105;
Best Local Similarity 32.7%; Pred. No. 1.6e-05;
Matches 34; Conservative 24; Mismatches 39; Indels 7; Gaps 5

Qy      8 PSVLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQY 66
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :
Db      6 PLVTLFPLSLKN-LQPTR-FQLCLVSE--FYPTLVVDVWVKDGVPTQGVETTPSQKQT 61
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :

Qy      67 NSTYRVVSVTLVHLQDWLNKGKEYCKYKSVNKGKLPSSIEKTIKAK 110
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :
Db      62 NNKYWVSSYLTLTSDQWPHSRYSRYVTHEG--NTVEKSVSPAE 103
      ||||| ||||| : : : : : || : : : : : || : : : : : || : : : : :

RESULT 9
S26653
Ig kappa chain C region - chimpanzee (fragment)
C/Species: Pan troglodytes (chimpanzee)
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C/Accession: S26653
R/Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A/Title: Potential of primate monoclonal antibodies to substitute for human an
A/Reference number: S26652; MUID:91355693; PMID:2129418
A/Accession: S26653
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-99 <EHR>

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.8539 Seconds
(without alignments)
723.518 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGBSPFLFPKPXKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	22.3	106	1 KAC_HUMAN	P01834 homo sapien
2	130	22.1	103	1 LAC_CHICK	P20763 gallus gall
3	121.5	20.7	105	1 LAC1_MOUSE	P01843 mus musculus
4	121.5	20.7	105	1 LAC5_MOUSE	P20765 mus spretus
5	117.5	20.0	105	1 LAC5_MOUSE	P20764 mus musculus
6	112.5	19.2	106	2 Q8TCJ5	Q8tcj5 homo sapien
7	112	19.1	103	1 KAC4_RABIT	P01840 oryctolagus
8	109.5	18.7	105	1 LAC_HUMAN	P01842 homo sapien
9	108.5	18.5	105	1 LAC_RABIT	P01847 oryctolagus
10	104	17.7	104	1 KAC6_RABIT	P03984 oryctolagus
11	103	17.5	106	1 KAC_MOUSE	P01837 mus musculus
12	101	17.2	104	1 LAC1_RAT	P20766 rattus norv
13	99.5	17.0	105	1 LAC_FIG	P01846 sus scrofa
14	98.5	16.8	106	1 KACB_RABIT	P01839 oryctolagus
15	95	16.2	104	1 LAC2_RAT	P20767 rattus norv
16	95	16.2	106	1 KACB_RAT	P01835 rattus norv
17	92.5	15.8	104	1 KAC9_RABIT	P01838 oryctolagus
18	92	15.7	103	1 KAC5_RABIT	P01841 oryctolagus
19	90	15.3	104	1 LAC3_MOUSE	P01845 mus musculus
20	90	15.3	106	1 KACA_RAT	P01836 rattus norv
21	76	12.9	104	1 LAC2_MOUSE	P01844 mus musculus
22	76	12.9	105	2 Q95JC1	Q95jc1 mus musculus
23	66	11.2	107	2 Q8KYI0	Q8kyi0 bacillus an
24	66	11.2	107	2 Q6EZI5	Q6ezi5 bacillus an
25	63	10.7	98	2 Q7XZF9	Q7xfz9 oryza sativ
26	62	10.6	93	2 Q6LBV9	Q6lbv9 mus musculus
27	61.5	10.5	91	2 Q6LBW2	Q6lbw2 mus musculus
28	61	10.4	93	2 Q9JKP1	Q9jkp1 marmota mon
29	60.5	10.3	74	2 P79659	P79659 oncorhynch
30	60.5	10.3	74	2 P79660	P79660 oncorhynch
31	60	10.2	73	2 Q8FBY4	Q8fby4 escherichia

32	59	10.1	79	1 SN5P_HUMAN	P80697 homo sapien
33	59	10.1	91	2 Q31248	Q31248 peromyscus
34	59	10.1	93	2 Q31158	Q31158 mus musculus
35	58.5	10.0	55	2 Q768W8	Q768w8 mus musculus
36	58.5	10.0	93	2 O19471	O19471 mus musculus
37	58.5	10.0	93	2 O19472	O19472 mus musculus
38	58.5	10.0	93	2 Q9QUH8	Q9quh8 mus musculus
39	58	9.9	103	2 Q8HX76	Q8hx76 sus scrofa
40	58	9.9	104	2 Q8C5T6	Q8c5t6 mus musculus
41	58	9.9	106	2 Q31261	Q31261 rattus norv
42	57.5	9.8	55	2 Q768W5	Q768w5 mus musculus
43	57.5	9.8	65	1 DN71_SULAC	P13123 sulfolobus
44	57.5	9.8	95	1 DAFI_TRYCR	Q26327 trypanosoma
45	57	9.7	90	1 ALB2_SULTO	Q971t6 sulfolobus

ALIGNMENTS

RESULT 1

KAC_HUMAN

ID KAC_HUMAN STANDARD; PRT; 106 AA.

AC P01834;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE IG kappa chain C region.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE (MYELOMA PROTEIN EU).

RX MEDLINE=71064023; PubMed=5489770;

RA Gortlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BONDS.

RX MEDLINE=71064027; PubMed=4923144;

RA Gall W.E., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";

RL Biochemistry 9:3188-3196(1970).

RN [3]

RP SEQUENCE (BENCE-JONES PROTEIN TI).

RX MEDLINE=72188439; PubMed=5027703;

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";

RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;

RA Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;

RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";

RL Cell 22:197-207(1980).

RN [5]

RP SEQUENCE (BENCE-JONES PROTEIN ROY).

RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;

RL (In) Franek F., Shugar D. (eds.);

RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).

RN [6]

RP SEQUENCE (BENCE-JONES PROTEIN CUM).

RX MEDLINE=68242259; PubMed=5586923;

RA Hilschmann N.;


```
Query Match      22.1%; Score 130; DB 1; Length 103;
Best Local Similarity 31.2%; Pred. No. 3.5e-05;
Matches 34; Conservative 25; Mismatches 42; Indels 8; Gaps 6;

QY 2 PPVAGGPFLEPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
DB 2 PKVA--PTTLPPPS--KEELNATKATLVCLINDF--YPSP-VTVDWVIDG--STRSGETTA 55
QY 62 REEQNSTYRVSVLTFLVQLDQLNGKEYKCKVSNKGLPSSIEKTISKAK 110
DB 56 PQQNSQNYWASSYLSASDSSSHETTCRVTHNG--TSIYTKLRSE 102

RESULT 3
LAC1_MOUSE
ID LAC1_MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Selsing E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=8114806; PubMed=6259534;
RA Botwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Geffer M.L., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL Nature 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=82220143; PubMed=6283385;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC -!- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
CC normal lambda-2 chain and 1 abnormal lambda-1 chain that is
CC missing a large part of the V region. The C region sequence (shown
CC here) appears completely normal.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; J00592; AAA51636.1; -
CC DR EMBL; J00597; AAB59672.1; -
CC PIR; A93922; L1MS.
CC PDB; 1JNH; X-ray; A=1-105.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
```

```
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS0290; IG_MHC; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
FT CONFLICT 19 20
FT CONFLICT 56 56
FT CONFLICT 75 75
FT CONFLICT 81 82
FT CONFLICT 85 85
FT CONFLICT 96 96
FT STRAND 4 4
FT STRAND 7 7
FT STRAND 10 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 52 54
FT STRAND 58 60
FT TURN 61 63
FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; A89F2B09BCFCA018 CRC64;

Query Match      20.7%; Score 121.5; DB 1; Length 105;
Best Local Similarity 31.1%; Pred. No. 0.00025;
Matches 32; Conservative 18; Mismatches 46; Indels 7; Gaps 3;

QY 8 PSVLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQ 66
DB 6 PSVTLFPSSSEEL-----ETNKATLVCTITDFYGVVTVDMKVDGTPVTQGMETTPQSKS 61
QY 67 NSTYRVSVLTFLVQLDQLNGKEYKCKVSNKGLPSSIEKTISKAK 109
DB 62 NKKYMASSYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSR 102

RESULT 4
LACS_MOUSE
ID LACS_MOUSE STANDARD; PRT; 105 AA.
AC P20765;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-5 chain C region.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88196070; PubMed=3129289;
RA Mami F., Cazenave P.A., Kindt T.J.;
RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
RL EMBO J. 7:117-122(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
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CC -----
CC EMBL; M35582; AAA39152.1; -.
CC HSP; P01843; IJNH.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig_c1.
CC DR InterPro; IPR003006; Ig_MHC.
CC PFam; PF00047; Ig; 1.
CC SMART; SM00407; Igc1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
FT SEQUENCE 105 AA; 11674 MW; 11674 MW; AAB417DF68471A17 CRC64;
Query Match 20.7%; Score 121.5; DB 1; Length 105;
Best Local Similarity 30.8%; Pred. No. 0.00025;
Matches 32; Conservative 22; Mismatches 43; Indels 7; Gaps 3;
QY 8 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREQY 66
Db 6 PLVTFLFSLKLN-----QANKVTLVCLVSEFPYPTGLVVDWKVDGVPVTTQGVETTPSKQT 61
QY 67 NSTYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 110
Db 62 NKKYMWSSYLTLLISDQWPHSRVTSCTVTHEG--NTVEKSVSPA 103
RESULT 5
LAC5 MOUSE
ID LAC5 MOUSE STANDARD; PRT; 105 AA.
AC P20764;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-5 chain C region.
GN Name=Igl-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065143; PubMed=3024017;
RA Sakaguchi N., Melchers F.;
RT "Lambda 5, a new light-chain-related locus selectively expressed in
RT pre-B lymphocytes."
RL Nature 324:579-582 (1986).
CC -!- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M30387; -; NOT_ANNOTATED_CDS.
CC HSP; P01843; IJNH.
CC MGB; MGI:96529; Igl-5.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig_c1.
CC DR InterPro; IPR003006; Ig_MHC.
CC SMART; SM00407; Igc1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE NEG.
CC KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 105 AA; 11674 MW; 11674 MW; AAB417DF68471A17 CRC64;
Query Match 20.7%; Score 121.5; DB 1; Length 105;
Best Local Similarity 30.8%; Pred. No. 0.00025;
Matches 32; Conservative 22; Mismatches 43; Indels 7; Gaps 3;
QY 8 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREQY 66
Db 6 PLVTFLFSLKLN-----QANKVTLVCLVSEFPYPTGLVVDWKVDGVPVTTQGVETTPSKQT 61
QY 67 NSTYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 110
Db 62 NKKYMWSSYLTLLISDQWPHSRVTSCTVTHEG--NTVEKSVSPA 103
RESULT 6
O8TCJ5
ID O8TCJ5 PRELIMINARY; PRT; 106 AA.
AC O8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp667J0810 (Fragment).
GN Name=DKFZp667J0810;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR HSP; P01842; IJNL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR PFam; PF07654; C1-set; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;
Query Match 19.2%; Score 112.5; DB 2; Length 106;
Best Local Similarity 28.7%; Pred. No. 0.002;
Matches 29; Conservative 22; Mismatches 43; Indels 7; Gaps 4;
QY 8 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPREQY 66
Db 7 PSVTLFPPSSE--LQANKATLVCLISD--FYPGAVTVAKADSSPVKAGVETTTPSKQS 62
QY 67 NSTYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIK 107
Db 63 NKKYAASSYLSLTPEQNKSHKSYSCQVTHEG--STVEKTV 101
RESULT 7
KAC4 RABIT
ID KAC4 RABIT STANDARD; PRT; 103 AA.
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8330036; PubMed=6412231;
RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
allotype J-C locus and evidence for several b4-related sequences in
the rabbit genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S., Kindt T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
to streptococcal carbohydrate. II. Sequence determination of peptides
from tryptic and peptic digests.";
RL J. Biol. Chem. 250:3289-3296(1975).
CC -!- MISCELLANEOUS: This chain was obtained from antibody to the
specific carbohydrate of group C Streptococci and was isolated
from the serum of a single rabbit.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; X00231; CAA25051.1; -.
DR PIR; A93971; K4RB.
DR HSP; P01837; 1KCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 5 95 Ig-like.
FT DISULFID 26 85 Interchain (with a heavy chain).
FT DISULFID 103 103 N -> D (in Ref. 3).
FT CONFLICT 58 58
SQ SEQUENCE 103 AA; 11043 MW; 5FC5AC8B60E68DB CRC64;
Query Match 19.1%; Score 112; DB 1; Length 103;
Best Local Similarity 31.4%; Pred. No. 0.0021;
Matches 33; Conservative 19; Mismatches 39; Indels 14; Gaps 6;
QY 3 PVAGPSVFLPPPKDILMSRTEVTCVVVDVSHEDPEVKFNYYDGV-----VHNAK 58
DB 2 PVA--PTVLIPPAADQ--VATGTVTIVCV---ANKYFPDVTVTWEVDGTTQTGTIENK 54
QY 59 TKPREQYNSTRVSVLTVLHODVNGKCYKCKVSKNGLPSSIE 103
DB 55 TP--QNSADCTYNLSSTLTLTSTQNSHKEYTKVT-QGTSVVQ 96
RESULT 8
LAC_HUMAN
ID LAC_HUMAN STANDARD; PRT; 105 AA.
AC P01842; P80423;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda chain C regions.
GN Name=IGLC1;
GN and
GN Name=IGLC2;
GN and
GN Name=IGLC3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN SH).
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
complete amino acid sequence and the location of the disulfide
bridges.";
RL J. Biol. Chem. 245:2171-2176(1970).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX MEDLINE=6908380; PubMed=4883841;
RA Milestein C., Clegg J.B., Jarvis J.M.;
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
Bence-Jones protein.";
RL Biochem. J. 110:631-652(1968).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
immunoglobulins. IV. Assignment of a suba subgroup.";
RL J. Biochem. 93:421-429(1983).
RN [4]
RP SEQUENCE (BENCE-JONES PROTEIN KERN).
RX MEDLINE=71150336; PubMed=5549568;
RA Ponstingl H., Hess M., Hilschmann N.;
RT "Structural rule of antibodies. Primary structure of a monoclonal
immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
protein Kern). V. The complete amino acid sequence and its genetic
interpretation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN [5]
RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX MEDLINE=74103253; PubMed=4814727;
RA Chen B.L., Poljak R.J.;
RT "Amino acid sequence of the (lambda) light chain of a human myeloma
immunoglobulin (IgG New).";
RL Biochemistry 13:1295-1302(1974).
RN [6]
RP SEQUENCE (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX MEDLINE=75046825; PubMed=4215080;
RA Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA Saul F.;
RT "The three-dimensional structure of the fab' fragment of a human
myeloma immunoglobulin at 2.0-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN [8]
RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX MEDLINE=75013804; PubMed=4415202;
RA Fett J.W., Deutsch H.F.;
RT "Primary structure of the MCG lambda chain.";
RL Biochemistry 13:4102-4114(1974).


```
Matches 29; Conservative 21; Mismatches 47; Indels 7; Gaps 4;
QY 8 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPRERQY 66
Db 6 PSVILFPPSPSEB--LKDNKATLVCLISDFYPR--TVKNWKKADGNSVTQGVDTTQPSKQS 61
QY 67 NSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
Db 62 NNKYAASSFLHLTANQWKSQSVTCQVTHEG--HTVEKSLAPAE 103

RESULT 10
KAC6_RABIT
ID KAC6_RABIT STANDARD; PRT; 104 AA.
AC P03984;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Ig kappa chain b5 variant C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (CLONE PKB5-F2).
RX MEDLINE=84041515; PubMed=6314281;
RA Bernstein K.E., Skurja R.M. Jr., Mage R.G.;
RT "The sequences of rabbit kappa light chains of b4 and b5 allotypes
RT differ more in their constant regions than in their 3' untranslated
RT regions."
RL Nucleic Acids Res. 11:7205-7214 (1983).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=6424123;
RA Emorine L., Sogn J.A., Trinh D., Kindt T.J., Max E.E.;
RT "A genomic gene encoding the b5 rabbit immunoglobulin kappa constant
RT region: implications for latent allotype phenomenon."
RL Proc. Natl. Acad. Sci. U.S.A. 81:1789-1793 (1984).
CC -!- MISCELLANEOUS: The cDNA from which this sequence was derived
CC contains a terminator codon within the V-region coding region. The
CC origin of this codon and of the differences between this and other
CC sequenced b5 C regions are unclear. The cDNA clone was made using
CC mRNA from trypanosome-infected b5-homozygous rabbits.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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EMBL; X00032; -; NOT ANNOTATED_CDS.
DR EMBL; K01363; AAA31355.1; -;
DR PIR; A02124; K5REV.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
DR KX Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 100 Ig-like.
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
FT CONFLICT 1 1 A -> VA (in Ref. 2).
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 17.7%; Score 104; DB 1; Length 104;
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Best Local Similarity 26.7%; Pred. No. 0.014;
Matches 28; Conservative 24; Mismatches 41; Indels 12; Gaps 5;
QY 8 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG----VEVHNAKTKPRE 63
Db 5 PTVILFPPSPAE--LATGTATIVCV--ANKYFPDGTVTWQVDGKPLTTGIETSKTPQNS 59
QY 64 EOYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIK 108
Db 60 D--DCTYNLSLTLLKSDYNSHDEYTCQVA--QSGSPVVOFSFR 101

RESULT 11
KAC_MOUSE
ID KAC_MOUSE STANDARD; PRT; 106 AA.
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain."
RL Biochem. J. 128:427-444 (1972).
RN [2]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=7308889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein."
RL Biochem. J. 126:837-850 (1972).
RN [3]
RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625; DOI=10.1016/0092-8674(78)90290-8;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
RT immunoglobulin mRNA using the dideoxynucleotide method of RNA
RT sequencing."
RL Cell 15:1067-1075 (1978).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing."
RL Nucleic Acids Res. 9:4485-4494 (1981).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
RT mouse kappa immunoglobulin J and C region genes."
RL J. Biol. Chem. 256:5116-5120 (1981).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RT kappa chain."
RL Nucleic Acids Res. 9:971-981 (1981).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
RA de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RT phosphatase."
RL Eur. J. Biochem. 176:287-295 (1988).
```


CC -!- MISCELLANEOUS: This chain was obtained from a mixture of normal immunoglobulins.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02129; L1PG.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 2 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match 17.0%; Score 99.5; DB 1; Length 105;
Best Local Similarity 27.6%; Pred. No. 0.039;
Matches 29; Conservative 20; Mismatches 47; Indels 9; Gaps 4;

QY 8 PSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA--KTPRREQ 65
DB 6 PTVNLFPSSSEEL-----GTNKAFLVCLISDFYPGAATVTWKAGGTTVVGVEETKRP-SKQ 60

QY 66 VNSTYRVVSVLTVLHQLDNLNGKEYKCKVSKNKLPSLSIEKTSKAK 110
DB 61 SNKKAASLYALSADKSSSGFTCVTHEG--TIVEKTVTPSE 103

RESULT 14
KACB_RABIT STANDARD; PRT; 106 AA.
ID KACB_RABIT
AC P01839;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG kappa-b4 chain C region.
GN Name=K-BAS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Basilea;
RX PubMed=11894960;
RA Heidmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
RL EMBO J. 2:437-441(1983).
CC -!- MISCELLANEOUS: In Basilea rabbits, the major type of light chain is lambda. The kappa chain shown is a minor component. All other rabbit B allotypes have Cys-64.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; V01241; CAA24558.1; -;
DR EMBL; V00885; -; NOT_ANNOTATED_CDS.
DR PIR; A02121; K4REBS.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 87
FT DISULFID 106 106 Interchain (with a heavy chain).
SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 16.8%; Score 98.5; DB 1; Length 106;
Best Local Similarity 29.1%; Pred. No. 0.049;
Matches 32; Conservative 21; Mismatches 44; Indels 13; Gaps 6;

QY 3 PVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE----VHNAK 58
DB 3 PVA--PSVLLFPSSKEE--LTGTATIVCVANKFYPSD--ITVTWKVDGTTQQSGIENSK 56

QY 59 TKPREEQYNSTYRVVSVLTVLHQLDNLNGKEYKCKVSKNKLPSLSIEKTSK 108
DB 57 TPQSPE--DNTYSLSSTLSLTSQAQYNHSHSVYTCEVV--QGSASPIVQSFNR 103

RESULT 15
LAC2_RAT STANDARD; PRT; 104 AA.
ID LAC2_RAT
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG lambda-2 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene."
RL Gene 55:75-84(1987).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M22521; AAA41420.1; ALT_INIT.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
SQ SEQUENCE 104 AA; 11318 MW; F087906DE43F7276 CRC64;

Query Match 16.2%; Score 95; DB 1; Length 104;
Best Local Similarity 21.4%; Pred. No. 0.11;
Matches 22; Conservative 27; Mismatches 48; Indels 6; Gaps 3;

QY 8 PSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREQN 67

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.6073 Seconds
(without alignments)
347.833 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APVAGGPSVFLPPPKPKDT.....CKVSNKGLPSSTIKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	94.9	110	3	US-08-444-644-21
2	557	94.9	110	3	US-08-232-246A-21
3	553	94.2	110	3	US-08-444-644-44
4	553	94.2	110	3	US-08-232-246A-44
5	549	93.5	109	2	US-08-070-116A-4
6	549	93.5	109	4	US-08-557-050-4
7	543.5	92.6	109	3	US-08-444-644-30
8	543.5	92.6	109	2	US-08-232-246A-30
9	541	92.2	105	2	US-08-232-539D-60
10	533	90.8	110	3	US-08-444-644-38
11	533	90.8	110	3	US-08-232-246A-38
12	344	58.6	66	3	US-08-569-147-85
13	175	29.8	107	4	US-09-281-760B-36
14	166.5	28.4	106	2	US-08-232-539D-54
15	152	25.9	109	3	US-08-466-163B-1
16	152	25.9	109	4	US-09-802-096-1
17	152	25.9	109	4	US-09-802-077-1
18	141	24.0	100	1	US-08-422-091-10
19	141	24.0	100	1	US-08-422-091-10
20	141	24.0	100	2	US-08-422-092-10
21	141	24.0	100	2	US-08-788-800-7
22	141	24.0	100	3	US-08-422-093-10
23	141	24.0	100	3	US-08-422-112-10
24	131.5	22.4	109	2	US-08-646-981-6
25	131	22.3	105	3	US-09-025-769B-166
26	131	22.3	105	4	US-09-490-070A-166
27	131	22.3	105	4	US-09-490-153-166

28 131 22.3 105 4 US-09-490-324-166 Sequence 166, App
29 131 22.3 106 2 US-08-378-939-40 Sequence 40, Appl
30 131 22.3 106 2 US-08-761-277A-49 Sequence 49, Appl
31 131 22.3 106 3 US-08-444-644-26 Sequence 26, Appl
32 131 22.3 106 3 US-08-232-246A-26 Sequence 26, Appl
33 131 22.3 107 1 US-08-422-101-8 Sequence 8, Appl
34 131 22.3 107 1 US-08-422-091-8 Sequence 8, Appl
35 131 22.3 107 2 US-08-422-092-8 Sequence 8, Appl
36 131 22.3 107 2 US-08-788-800-5 Sequence 5, Appl
37 131 22.3 107 3 US-08-422-093-8 Sequence 8, Appl
38 131 22.3 107 3 US-08-422-112-8 Sequence 8, Appl
39 131 22.3 107 3 US-09-301-593-20 Sequence 20, Appl
40 131 22.3 108 4 US-09-313-942-13 Sequence 13, Appl
41 129 22.0 106 1 US-08-399-106A-7 Sequence 7, Appl
42 129 22.0 106 1 US-08-433-105A-7 Sequence 7, Appl
43 129 22.0 106 2 US-08-434-869A-7 Sequence 8, Appl
44 128 21.8 109 1 US-08-436-463-8 Sequence 8, Appl
45 128 21.8 109 1 US-08-024-253-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-21

Query Match          94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 2
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match          94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 3
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-44

Query Match          94.2%; Score 553; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 6.2e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
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RESULT 4
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALX88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-44

Query Match 94.2%; Score 553; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 6.2e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 61 PREEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 5
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
```

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; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-116A-4

Query Match 93.5%; Score 549; DB 2; Length 109;
Best Local Similarity 94.5%; Pred. No. 1.8e-57;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 PPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 61
Db 1 PEFLLGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 62 REEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 REEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 6
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match          93.5%; Score 549; DB 4; Length 109;
Best Local Similarity 94.5%; Pred. No. 1.8e-57;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 PVVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 1 PEFGLGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

QY 62 REEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIISKAK 109

RESULT 7
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 601555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match          92.6%; Score 543.5; DB 3; Length 109;
Best Local Similarity 92.7%; Pred. No. 8.3e-57;
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 APPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59

QY 61 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 60 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPAPIEKTIISKTK 109

RESULT 8
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
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; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-232-246A-30

Query Match          92.6%; Score 543.5; DB 3; Length 109;
Best Local Similarity 92.7%; Pred. No. 8.3e-57;
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59

QY 61 PREEOYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
Db 60 PREEQNSTFRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKTK 109

RESULT 9
US-08-232-539D-60
; Sequence 60, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-232-539D-60

Query Match          92.2%; Score 541; DB 2; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.6e-56;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 66

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-444-644-38

Query Match          90.8%; Score 533; DB 3; Length 110;
Best Local Similarity 90.9%; Pred. No. 1.5e-55;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPELLGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREEOYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
Db 61 LREEOYNSTFRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-444-644-38

Query Match          90.8%; Score 533; DB 3; Length 110;
Best Local Similarity 90.9%; Pred. No. 1.5e-55;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPELLGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREEOYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
Db 61 LREEOYNSTFRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110
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, NUMBER OF SEQUENCES: 95
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
, ADDRESSEE: No. 6180377rie, LLP
, STREET: One Liberty Place - 46th Floor
, CITY: Philadelphia
, STATE: PA
, COUNTRY: U.S.A.
, ZIP: 19103
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/569,147
, FILING DATE: 25-March-1996
, CLASSIFICATION: 536
, ATTORNEY/AGENT INFORMATION:
, NAME: Trujillo, Doreen Yatio
, REGISTRATION NUMBER: 35,719
, REFERENCE/DOCKET NUMBER: CARP-0047
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (215) 568-3100
, TELEFAX: (215) 568-3439
, INFORMATION FOR SEQ ID NO: 85:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 66 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-569-147-85

Query Match 58.6%; Score 344; DB 3; Length
Best Local Similarity 95.5%; Pred. No. 28-33;
Matches 63; Conservative 1; Mismatches 2; Indel

Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
||| : |||||
Db 1 APELLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
||| : |||||

Qy 61 PREEQY 66
|||
Db 61 PREEQY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature

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RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-232-246A-38

Query Match 90.8%; Score 533; DB 3; Length 110;
Best Local Similarity 90.9%; Pred. No. 1.5e-55;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKQDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   || : |||||
Db 1 APELLGGPSVFLPPPKQDTLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
   || : |||||

QY 61 PREEQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   |||||
Db 61 LRBEQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES

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; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: "n" stands for any nucleic acid
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; NAME/KEY: misc feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
; OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-36

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Query Match 29.8%; Score 175; DB 4; Length 107;
Best Local Similarity 35.0%; Pred. No. 4.3e-13;
Matches 36; Conservative 23; Mismatches 42; Indels 2; Gaps 2;

QY 7 GPSVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQY 66
Db 5 GVSAYLSRPPSPD-LVYHKAPKITCLVLDLATWE-GMNLTYRESKEPVNPPVLPNKKDHF 62

QY 67 NSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKA 109
Db 63 NGTITVTSTLPVNTDWDIEGETYQCRVTHPLPDMRSTTK 101

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RESULT 14
US-08-232-539D-54
; Sequence 54, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-54

Query Match 28.4%; Score 166.5; DB 2; Length 106;
Best Local Similarity 34.3%; Pred. No. 4.4e-12;
Matches 35; Conservative 22; Mismatches 44; Indels 1; Gaps 1;

QY 7 GPSVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQY 66
Db 1 GVSAYLSRPPSPD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEKQR 59

QY 67 NSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIK 108
Db 60 NGTITVTSTLPVNTDWDIEGETYQCRVTHPLPDMRSTTK 101

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RESULT 15
US-08-466-163B-1
; Sequence 1, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-1

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Query Match 25.9%; Score 152; DB 3; Length 109;
Best Local Similarity 34.3%; Pred. No. 2.4e-10;
Matches 35; Conservative 21; Mismatches 44; Indels 2; Gaps 2;

QY 7 GPSVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQY 66
Db 6 GVSAYLSRPPSPD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEKQR 64

QY 67 NSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIK 108

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Db 65 NGTLTVTSLPVGTRDWIEG-ETQCRVTHPHLPRLMRSTTK 105

Search completed: November 17, 2005, 07:53:56
Job time : 24.6073 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 83.1279 Seconds
(without alignments)
553.666 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLPPPKPKDT.....CKVSNKGLPSSTKTSKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	579	98.6	110	18	US-10-959-318-9
2	579	98.6	110	18	US-10-959-318-10
3	565	96.3	110	18	US-10-959-318-13
4	565	96.3	110	18	US-10-959-318-14
5	563	95.9	110	18	US-10-959-318-7
6	563	95.9	110	18	US-10-959-318-8
7	562.5	95.8	109	18	US-10-959-318-11
8	562.5	95.8	109	18	US-10-959-318-12
9	561	95.6	110	20	US-11-018-102-23
10	559	95.2	110	20	US-11-018-102-25
11	558	95.1	109	18	US-10-627-556-270

12	557	94.9	110	15	US-10-370-749-23	Sequence 23, Appl
13	557	94.9	110	18	US-10-959-318-1	Sequence 1, Appl
14	557	94.9	110	20	US-11-018-102-22	Sequence 22, Appl
15	553	94.2	109	14	US-10-207-655-220	Sequence 14, Appl
16	553	94.2	109	18	US-10-627-556-14	Sequence 220, Appl
17	553	94.2	110	18	US-10-959-318-4	Sequence 4, Appl
18	553	94.2	110	18	US-10-959-318-21	Sequence 21, Appl
19	553	94.2	110	20	US-11-018-102-24	Sequence 24, Appl
20	552	94.0	109	14	US-10-020-354-80	Sequence 80, Appl
21	552	94.0	110	15	US-10-370-749-53	Sequence 53, Appl
22	550	93.7	110	15	US-10-370-749-51	Sequence 51, Appl
23	550	93.7	110	18	US-10-959-318-22	Sequence 22, Appl
24	549	93.5	109	14	US-10-267-286A-4	Sequence 4, Appl
25	549	93.5	109	18	US-10-627-556-294	Sequence 294, Appl
26	549	93.5	110	18	US-10-959-318-5	Sequence 5, Appl
27	549	93.5	110	18	US-10-959-318-6	Sequence 6, Appl
28	549	93.5	110	18	US-10-959-318-25	Sequence 25, Appl
29	548.5	93.4	109	18	US-10-959-318-15	Sequence 15, Appl
30	548.5	93.4	109	18	US-10-959-318-16	Sequence 16, Appl
31	548	93.4	109	18	US-10-627-556-258	Sequence 258, App
32	548	93.4	109	18	US-10-627-556-278	Sequence 278, App
33	548	93.4	109	18	US-10-627-556-302	Sequence 302, App
34	548	93.4	110	18	US-10-959-318-23	Sequence 23, Appl
35	548	93.4	110	18	US-10-959-318-24	Sequence 24, Appl
36	547	93.2	110	17	US-10-491-653-22	Sequence 22, Appl
37	545	92.8	109	14	US-10-207-655-322	Sequence 322, App
38	545	92.8	109	18	US-10-627-556-92	Sequence 92, Appl
39	543.5	92.6	109	18	US-10-959-318-2	Sequence 2, Appl
40	539	91.8	110	18	US-10-959-318-3	Sequence 3, Appl
41	535.5	91.2	109	18	US-10-959-318-17	Sequence 17, Appl
42	535.5	91.2	109	18	US-10-959-318-18	Sequence 18, Appl
43	532	90.6	109	18	US-10-627-556-286	Sequence 286, App
44	531	90.5	110	18	US-10-959-318-19	Sequence 19, Appl
45	531	90.5	110	18	US-10-959-318-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-10-959-318-9

; Sequence 9, Application US/10959318

; Publication No. US20050215768A1

; GENERAL INFORMATION:

; APPLICANT: Armour, Kathryn L

; APPLICANT: Clark, Michael R

; TITLE OF INVENTION: Polypeptides including modified constant regions

; FILE REFERENCE: 39-302

; CURRENT APPLICATION NUMBER: US/10/959,318

; CURRENT FILING DATE: 2004-10-07

; PRIOR APPLICATION NUMBER: PCT/GB2004/004254

; PRIOR FILING DATE: 2004-10-07

; PRIOR APPLICATION NUMBER: GB0324368.0

; PRIOR FILING DATE: 2003-10-17

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 9

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)

US-10-959-318-9

Query Match 98.6%; Score 579; DB 18; Length 110;

Best Local Similarity 99.1%; Pred. No. 1.1e-48;

Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

DB 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Qy	61 PREEQYNSTYRWWSVLTVLHQDWLNGKEYCKVSNKGIPSSIEKTIISKAK 110
D6	61 PREEQYNSTYRWWSVLTVLHQDWLNGKEYCKVSNKGIPSSIEKTIISKAK 110

```

RESULT 2
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a,
; OTHER INFORMATION: mutations
US-10-959-318-10

```

```

RESULT 3
US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-13

```

Query Match	96.3%	Score 565;	DB 18;	Length 110;
Best Local Similarity	96.4%	Pred. No. 2.4e-47;		
Matches 106; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	1	APVACGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK	60
Db	1	APVACGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK	60
Qy	61	PREQYNSTRYRVSVLTVLHQDLNGKEYCKVSNKGIPSSIEKTSISK	110
Db	61	PREQYNSTRYRVSVLTVLHQDLNGKEYCKVSNKALPAPTEKTSISK	110

```

RESULT 4
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: FCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c
; OTHER INFORMATION: mutations
US-10-959-318-14

```

```

RESULT 5
US-10-959-318-7
; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a
; OTHER INFORMATION: mutations

```

; LENGTH: 110

```
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: engineered G1 CH2
US-11-018-102-23

Query Match          95.6%; Score 561; DB 20; Length 110;
Best Local Similarity 95.5%; Pred. No. 6e-47;
Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||
Db 1 APEAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   |||||
Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

RESULT 10
US-11-018-102-25
; Sequence 25, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018,102
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: engineered G4 CH2
US-11-018-102-25

Query Match          95.2%; Score 559; DB 20; Length 110;
Best Local Similarity 95.5%; Pred. No. 9.4e-47;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||
Db 1 APEAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   |||||
Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110

RESULT 11
US-10-627-556-270
; Sequence 270, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 270
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-10-627-556-270

Query Match          95.1%; Score 558; DB 18; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.2e-46;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 61
   |||||
Db 1 PELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 62 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   |||||
Db 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109

RESULT 12
US-10-370-749-23
; Sequence 23, Application US/10370749
; Publication No. US20040002587A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Allan, Barrett
; TITLE OF INVENTION: FC Region Variants
; FILE REFERENCE: AMB-07823
; CURRENT APPLICATION NUMBER: US/10/370,749
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/358,161
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-370-749-23

Query Match          94.9%; Score 557; DB 15; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.5e-46;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||
Db 1 APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   |||||
Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

RESULT 13
US-10-959-318-1
; Sequence 1, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 91.6667 Seconds
(without alignments)
464.112 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGSPVLPFPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqpl980s:.*
2: Geneseqpl990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	97.8	437	7 ADM33855	Adm33855 Human HuE
2	570	97.8	437	8 ADR48986	Adr48986 HuBPO-L-v
3	570	97.8	449	7 ADM33378	Adm33378 Human GCS
4	566.5	97.2	462	2 AAW14933	Aaw14933 2A2 (Chim
5	566.5	97.2	462	2 AAW14934	Aaw14934 2A2 (Chim
6	566.5	97.2	463	2 AAW14939	Aaw14939 3F4 (Chim
7	566.5	97.2	463	2 AAW14940	Aaw14940 3F4 (Chim
8	566.5	97.2	472	5 ABP51695	Abp51695 5G1.1-TP0
9	566.5	97.2	472	8 ADQ16647	Adq16647 Immunoglo
10	565	96.9	110	2 AAR41717	Aar41717 Undefined
11	565	96.9	218	3 AAB07478	Aab07478 Amino aci
12	565	96.9	218	4 AAB76425	Aab76425 Human IGG
13	565	96.9	218	4 AAB67205	Aab67205 Human IGG
14	565	96.9	218	5 AAG78436	Aag78436 Native se
15	565	96.9	218	6 ABR42442	AbR42442 Human IGG
16	565	96.9	218	8 ADH75380	Adh75380 Human IGG
17	565	96.9	229	7 ADD32013	Add32013 Heterolog
18	565	96.9	229	8 ADR48994	Adr48994 Human IGG
19	565	96.9	266	8 ADJ52121	Adj52121 CHI delet
20	565	96.9	284	6 AAE30927	Aae30927 Gly8-Glu2
21	565	96.9	327	2 AAW37346	Aaw37346 Immunoglo
22	565	96.9	327	5 AAM47859	Aam47859 Human IGG
23	565	96.9	327	6 AAE32918	Aae32918 Human imm
24	565	96.9	327	6 AAE32630	Aae32630 Human imm
25	565	96.9	327	6 AAO30892	Aao30892 Human imm

26	565	96.9	327	7 ADE97357	Ade97357 Human IGG
27	565	96.9	327	7 ADF75004	Adf75004 Human Ig
28	565	96.9	327	8 ADMA1543	Adm41543 Anti-inte
29	565	96.9	329	2 AAW70801	Aaw70801 Amino aci
30	565	96.9	329	3 AAY92190	Aay92190 Human IGG
31	565	96.9	329	7 ABW02169	Abw02169 Human Cga
32	565	96.9	329	8 ADL35097	Adl35097 Human IGG
33	565	96.9	330	6 ABR42735	AbR42735 Anti-ties
34	565	96.9	382	2 AAR90922	Aar90922 IL4.Y124D
35	565	96.9	382	2 AAR90921	Aar90921 IL4.Y124D
36	565	96.9	396	2 AAW10534	Aaw10534 Leptin 1-
37	565	96.9	396	2 AAW10535	Aaw10535 Leptin 1-
38	565	96.9	403	7 ADD32018	Add32018 Heterolog
39	565	96.9	432	2 AAY17903	Aay17903 Human IFN
40	565	96.9	433	2 AAW18579	Aaw18579 Interfero
41	565	96.9	443	2 AAW13564	Aaw13564 Humanised
42	565	96.9	444	2 AAY31672	Aay31672 Human IGG
43	565	96.9	444	6 ABR55342	AbR55342 Amino aci
44	565	96.9	444	7 ADC73234	Adc73234 Protein s
45	565	96.9	444	8 ADF69629	Adf69629 Humanized

ALIGNMENTS

RESULT 1
ADM33855
ID ADM33855 standard; protein; 437 AA.
XX ADM33855;
XX AC
XX AD
DT 03-JUN-2004 (first entry)
XX
DE Human HuBPO-L-vFcgamma4 fusion protein.
XX
KW Erythropoietin; EPO; immunoglobulin; IGG;
KW fragment crystallisation region; Fc; chronic anaemia; renal disease;
KW cancer chemotherapy; rheumatoid arthritis; AIDS;
KW myelodysplastic syndrome; (HuEPO)-L-vFcgamma4; human.
XX
OS Homo sapiens.
OS Synthetic.
XX

Key	Location/Qualifiers
Peptide	1..27
Protein	/note= "Signal peptide"
Protein	28..192
Protein	/note= "EPO"
Protein	193..208
Protein	/note= "Linker"
Protein	209..437
Misc-difference	/note= "IgG4 Fc"
Misc-difference	219
Misc-difference	/note= "Wild-type Ser substituted by Pro"
Misc-difference	226
Misc-difference	/note= "Wild-type Leu substituted by Ala"
US2003082749-A1.	
01-MAY-2003.	
17-AUG-2001; 2001US-00932812.	
17-AUG-2001; 2001US-00932812.	
(SUNL/) SUN L K.	
(SUNB/) SUN B N C.	
(SUNC/) SUN C R Y.	
Sun LK, Sun BNC, Sun CRV;	
WPI; 2003-616080/58.	
N-PSDB; ADM33854.	


```
CC sequence of human GCSF-L-fragment of crystallisation gamma 4 variant
CC fusion protein.
XX
XX Sequence 449 AA;
SQ
Query Match          97.8%; Score 570; DB 7; Length 449;
Best Local Similarity 98.2%; Pred. No. 8.2e-49;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY   1 APPVAGSPSVFLPPPKDKTLMISRPEVTVCVVVDVSQEDPVEQFNWYDGVVHNAKTK 60
    |||||
DB   233 AREFAGSPSVFLPPPKDKTLMISRPEVTVCVVVDVSQEDPVEQFNWYDGVVHNAKTK 292
    |||||
QY   61 PREEQNSTRYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTISKAK 110
    |||||
DB   293 PREEQNSTRYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTISKAK 342
    |||||

RESULT 4
AAWI14933
ID ID AAWI14933 standard; protein; 462 AA.
XX AC AC AAWI14933;
XX XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX XX
DE 2A2 (Chimeric) human G2/G4 chimeric antibody.
XX XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX XX
PN WO9711971-A1.
XX XX
PD 03-APR-1997.
XX XX
PF 27-SEP-1996; 96WO-USO15575.
XX XX
PR 28-SEP-1995; 95US-0004489P.
XX PR 26-SEP-1996; 96US-00004489.
XX XX (ALEX-) ALEXION PHARM INC.
XX PA Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
XX PI WPI; 1997-212855/19.
XX DR N-PSTDB; AAT62931.
XX DR
XX PT Antibodies binding to porcine but not human cell interaction proteins -
XX PT useful to treat and assay for rejection of xenografted porcine organs,
XX PT tissues or cells.
XX PS Disclosure; Page 42-44; 105pp; English.
XX XX
CC A chimeric antibody (AAWI14933) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (Mab) 2A2 heavy chain variable region sequence (see
CC also AAWI14932). The chimeric antibody is specific for porcine VCAM. It is
CC useful for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs into
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX XX
SQ Sequence 462 AA;
Query Match          97.2%; Score 566.5; DB 2; Length 462;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
 |||||
 Db 247 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 305
 |||||

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 |||||
 Db 306 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 355
 |||||

RESULT 5

AAW14934
 ID AAW14934 standard; protein; 462 AA.

XX AC AAW14934;
 DT 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX DE 2A2 (Chimeric) human G2/G4 chimeric antibody.
 XX KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX OS Homo; sapiens.
 OS Mus sp.
 OS Chimeric.
 XX PN WO9711971-A1.
 XX PD 03-APR-1997.
 XX PF 27-SEP-1996; 96WO-US015575.
 XX PR 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX PA (ALEX-) ALEXION PHARM INC.
 XX PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62932.

XX PT Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 XX PS Disclosure; Page 44-47; 105pp; English.
 XX CC A chimeric antibody (AAW14934) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (Mab) 2A2 heavy chain variable region sequence (see
 CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs into
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 462 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 462;
 Best Local Similarity 99.1%; Pred. No. 1.9e-48;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
 |||||
 Db 247 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 305
 |||||

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 |||||
 Db 306 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 355
 |||||

RESULT 7

AAW14940
 ID AAW14940 standard; protein; 463 AA.

XX AC AAW14940;
 DT 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX DE 3F4 (Chimeric) human G2/G4 chimeric antibody.
 XX KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX OS Homo; sapiens.
 OS Mus sp.
 OS Chimeric.
 XX PN WO9711971-A1.
 XX PD 03-APR-1997.
 XX PF 27-SEP-1996; 96WO-US015575.
 XX PR 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX PA (ALEX-) ALEXION PHARM INC.
 XX PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62932.

XX PT Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 XX PS Disclosure; Page 44-47; 105pp; English.
 XX CC A chimeric antibody (AAW14934) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (Mab) 2A2 heavy chain variable region sequence (see
 CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs into
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 463 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 463;
 Best Local Similarity 99.1%; Pred. No. 1.9e-48;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

RESULT 6

AAW14939
 ID AAW14939 standard; protein; 463 AA.

XX AC AAW14939;
 DT 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX DE 3F4 (Chimeric) human G2/G4 chimeric antibody.
 XX KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX OS Homo; sapiens.
 OS Mus sp.
 OS Chimeric.
 XX PN WO9711971-A1.
 XX PD 03-APR-1997.
 XX PF 27-SEP-1996; 96WO-US015575.
 XX PR 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX PA (ALEX-) ALEXION PHARM INC.
 XX PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62932.

XX PT Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 XX PS Disclosure; Page 56-57; 105pp; English.
 XX CC A chimeric antibody (AAW14939) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (Mab) 3F4 heavy chain variable region sequence (see
 CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs into
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 463 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 463;
 Best Local Similarity 99.1%; Pred. No. 1.9e-48;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
 |||||
 Db 248 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 306
 |||||

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 |||||
 Db 307 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 356
 |||||

RESULT 7

AAW14940
 ID AAW14940 standard; protein; 463 AA.

XX AC AAW14940;
 DT 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX DE 3F4 (Chimeric) human G2/G4 chimeric antibody.
 XX KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX OS Homo; sapiens.
 OS Mus sp.
 OS Chimeric.
 XX PN WO9711971-A1.
 XX PD 03-APR-1997.
 XX PF 27-SEP-1996; 96WO-US015575.
 XX PR 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX PA (ALEX-) ALEXION PHARM INC.
 XX PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62932.

XX PT Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 XX PS Disclosure; Page 56-57; 105pp; English.
 XX CC A chimeric antibody (AAW14939) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (Mab) 3F4 heavy chain variable region sequence (see
 CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs into
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 463 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 463;
 Best Local Similarity 99.1%; Pred. No. 1.9e-48;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
 |||||
 Db 248 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 306
 |||||

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 |||||
 Db 307 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 356
 |||||

```

DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
DE 3F4 (Chimeric) human G2/G4 chimeric antibody.
XX
XX Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX
XX WO9711971-A1.
XX
XX 03-APR-1997.
XX
XX 27-SEP-1996; 96WO-US015575.
XX
XX 28-SEP-1995; 95US-0004489P.
XX 26-SEP-1996; 96US-00004489.
XX (ALEX-) ALEXION PHARM INC.
XX
XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
XX WPI; 1997-212855/19.
XX N-PSDB; AAT62937.
XX
XX Antibodies binding to porcine but not human cell interaction proteins -
XX useful to treat and assay for rejection of xenografted porcine organs,
XX tissues or cells.
XX
XX Disclosure; Page 58-61; 105pp; English.
XX
XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of
XX human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAB) and a
XX murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
XX monoclonal antibody (MAB) 3F4 heavy chain variable region sequence (see
XX also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
XX useful for diagnosing human rejection of porcine xenotransplants and for
XX improving xenotransplantation of porcine cells, tissues and organs into
XX human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 463 AA;
Query Match 97.2%; Score 566.5; DB 2; Length 463;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 APPVAGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 248 APPVA-GPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 306
QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSKNKGKLPSSIEKTIKAK 110
DB 307 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSKNKGKLPSSIEKTIKAK 356
RESULT 8
ABP51695
ID ABP51695 standard; protein; 472 AA.
XX
XX ABP51695;
XX
XX 01-OCT-2002 (first entry)
XX
XX SG1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.
XX
XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX

```

```

OS Homo sapiens.
OS Synthetic.
XX
XX WO200246238-A2.
XX
XX 13-JUN-2002.
XX
XX 05-DEC-2001; 2001WO-US047656.
XX
XX 05-DEC-2000; 2000US-0251448P.
XX 04-MAY-2001; 2001US-0288889P.
XX 29-MAY-2001; 2001US-0294068P.
XX (ALEX-) ALEXION PHARM INC.
XX
XX Bowdish KS, Barbas-Frederickson S, Renshaw M;
XX WPI; 2002-566610/60.
XX N-PSDB; ABQ73374.
XX
XX A novel immunogen molecule comprising a region in which amino acid
XX residues corresponding to at least a portion of the complementary
XX determining region are replaced or fused with an erythropoietin or
XX thrombopoietin mimetic.
XX
XX Example 4; Fig 13A; 113pp; English.
XX
XX The present invention describes an immunoglobulin molecule or its fragment
XX (I) comprising a region where amino acid residues corresponding to at
XX least a portion of the complementary determining region (CDR) are
XX replaced or fused with biologically active peptides e.g. a peptide
XX mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
XX that is flanked with proline at its carboxy terminus. (I) has
XX antianaemic, haemostatic and nephrotropic activities, and can be used as
XX a stimulator of proliferation, differentiation and maturation of
XX haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
XX for stimulating proliferation, differentiation or growth of
XX promegakaryocytes or megakaryocytes, where (I) is contacted with
XX promegakaryocytes or megakaryocytes, which results in increased platelet
XX production. (I) with a region where amino acid residues corresponding to
XX a portion of CDR is replaced with an EPO mimetic, or which has one or
XX more of its CDRs fused to an EPO mimetic, is useful for increasing the
XX production of red blood cells, where (I) is contacted with haematopoietic
XX stem cells or their progenitors. (I) is useful for diagnostics or
XX therapeutics, in cell isolation strategies, and for treating patients
XX suffering from deficiency in cell populations caused by disease,
XX disorders or treatments related to the suppression of haematopoiesis.
XX ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
XX the exemplification of the present invention
XX
SQ Sequence 472 AA;
Query Match 97.2%; Score 566.5; DB 5; Length 472;
Best Local Similarity 99.1%; Pred. No. 2e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 APPVAGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 257 APPVA-GPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315
QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSKNKGKLPSSIEKTIKAK 110
DB 316 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSKNKGKLPSSIEKTIKAK 365
RESULT 9
ADQ16647
ID ADQ16647 standard; protein; 472 AA.
XX
XX ADQ16647;
XX
XX 09-SEP-2004 (first entry)
XX

```

DE Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67.
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW immunotherapy; thrombocytopenia.
XX Synthetic.
XX WO2004050017-A2.
XX 17-JUN-2004.
XX 17-NOV-2003; 2003WO-US036894.
XX 02-DEC-2002; 2002US-00307724.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Frederickson S, Renshaw M;
XX WPI; 2004-460973/43.
XX N-PSDB; ADQ16648.
XX New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX Example 4; SEQ ID NO 67; 107pp; English.
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents an immunoglobulin antibody heavy chain of
CC the invention.
XX
XX Sequence 472 AA;
Query Match 97.2%; Score 566.5; DB 8; Length 472;
Best Local Similarity 99.1%; Pred. No. 2e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 APPVAGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
Db 257 APPVA-GPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 315
QY 61 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 316 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 365
RESULT 10
AAR41717
ID AAR41717 standard; protein; 110 AA.
XX AAR41717;
XX
XX 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX Undefined ORF2 encoded by plasmid pAH4808.
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.

XX Synthetic.
OS WO9310819-A1.
XX 10-JUN-1993.
XX 24-NOV-1992; 92WO-US010206.
XX 26-NOV-1991; 91US-00800458.
XX (ALKE-) ALKERMES INC.
XX Friden PM;
XX WPI; 1993-196742/24.
XX N-PSDB; AAQ43848.
XX Antibody conjugates specific for transferrin receptor - used for
PT diagnosis and treatment of cancer, AIDS and neurological disorders.
XX Disclosure; Fig 19J; 151pp; English.
XX The sequences given in AAR41715-18 are encoded by the expression vector
CC pAH4808. This vector represents the cloning of the human gamma isotype,
CC gamma-4, with the variable region of the murine monoclonal antibody
CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the
CC heavy chain (VH) is derived from a murine source and the sequences
CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,
CC in combination with the chimeric light chain vector, pAG4611 (see also
CC AAQ33845), was transfected into SP2/0 cells and clones were isolated.
CC 128.1 is an anti-human transferrin receptor antibody which binds to the
CC transferrin receptor on brain capillary endothelial cells. This antibody
CC may be used in a conjugate in which it is linked to a neuropharmaceutical
CC or diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 110 AA;
Query Match 96.9%; Score 565; DB 2; Length 110;
Best Local Similarity 97.3%; Pred. No. 4.9e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 APPVAGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
Db 1 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
QY 61 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110
RESULT 11
AAB07478
ID AAB07478 standard; protein; 218 AA.
XX AAB07478;
XX 20-OCT-2000 (first entry)
XX Amino acid sequence of native IgG Fc region humIgG4.
XX IgG antibody; light chain; Fc region; effector function; cancer; allergy;
KW asthma; LFA-1-mediated disorder; tumour; cancer.
XX Homo sapiens.
XX WO200042072-A2.
PD 20-JUL-2000.
XX

XX Disclosure; Fig 2; 69pp; English.

XX The present invention relates to a fusion protein, comprising a peptide

CC ligand and an immunoglobulin (Ig) constant region multimerization domain

CC (1b). The hybrid molecules comprising the peptide ligands and their

CC functional derivatives can be used in the same applications as, a peptide

CC ligand can be used. For example the peptide ligand can bind ErbB2. The

CC peptide ligand may bind to and inhibit the activity associated with a

CC particular target molecule

XX Sequence 218 AA;

SQ

Query Match 96.9%; Score 565; DB 4; Length 218;

Best Local Similarity 97.3%; Pred. No. 1.1e-48;

Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

DB 2 APEFLGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

QY 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110

DB 62 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 111

RESULT 14

AAG78436

ID AAG78436 standard; protein; 218 AA.

XX AAG78436;

XX

XX 12-APR-2002 (first entry)

DT Native sequence human IgG Fc region sequence humIgG4.

DE

XX Antibody; antigen; immunoglobulin; ADCC; CDC; anti-globin response;

KW antibody dependant cell mediated cytotoxicity;

KW complement dependant cytotoxicity; epidermal growth factor receptor;

KW tumour necrosis factor; lymphocyte; tetraivalent antibody; cytostatic;

KW antiinflammatory; antipsoiatric; dermatological; antiulcer;

KW antiasthmatic; antiarteriosclerotic; antirheumatic; antibacterial;

KW antiarthritic; neuroprotective; immunosuppressive; antianaemic;

KW antiallergic; antidiabetic; gene therapy; human.

XX

XX Homo sapiens.

XX

XX WO200177342-A1.

FN

XX

XX 18-OCT-2001.

PD

XX

XX 20-MAR-2001; 2001WO-US008928.

PF

XX

XX 11-APR-2000; 2000US-0195819P.

PR

XX

XX (GETH) GENENTECH INC.

PA

XX

XX Miller KL, Presta LG;

PI

XX

XX WPI; 2002-049149/06.

DR

XX

XX Novel engineered antibody useful in therapeutic applications, contains a

PT dimerization domain and three or more antigen binding sites.

PT

XX Disclosure; Fig 3; 186pp; English.

PS

XX This invention relates to an isolated antibody comprising a dimerisation

CC domain and three or more antigen binding sites amino-terminal to the

CC domain. It is cytostatic, antiinflammatory, antibacterial,

CC immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used

CC in gene therapy. Along with a cytotoxic agent, is useful for treating a

CC disorder e.g. cancer in a mammal, for inducing apoptosis of a cancer

CC cell, and for killing a B cell or a cell which overexpresses or expresses

CC an ErbB receptor and for treating benign and malignant tumours,

CC inflammatory, angiogenic and immunological disorders, autoimmune

CC diseases, central nervous system inflammatory disorders. The antibody is

CC also useful for immunodiagnosis of various diseases including cancer, for

CC human therapy in redirected cytotoxicity, and also useful as fibrinolytic

CC agents or vaccine adjuvants, useful as affinity purification agent, in

CC diagnostic assays for detecting the expression of antigen of interest in

CC specific cells, tissue or serum, and useful for blocking an immune

CC response to a foreign antigen. The antigen is internalised faster than a

CC bivalent antibody by a cell expressing an antigen to which the antibodies

CC bind. The antibody comprises three or four heavy chain variable domains

CC which are able to combine with three or four light chain variable domain

CC polypeptides to form three or four antigen binding sites directed against

CC the same antigen. This sequence represents the native sequence human IgG

CC Fc region, humIgG4

XX

SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 5; Length 218;

Best Local Similarity 97.3%; Pred. No. 1.1e-48;

Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

DB 2 APEFLGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

QY 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110

DB 62 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 111

RESULT 15

ABR42442

ID ABR42442 standard; protein; 218 AA.

XX ABR42442;

XX

XX 11-AUG-2003 (first entry)

DT Human IgG4 Fc region.

DE

XX Human; antibody; IgG4; cytostatic; immunosuppressive; antiinflammatory;

KW antimicrobial.

KW

XX Homo sapiens.

XX

XX Key Location/Qualifiers

FH Misc-difference 153

FT

XX /note= "given as 'Z' in Fig 23"

XX

XX WO2003035835-A2.

PN

XX

XX 01-MAY-2003.

PD

XX

XX 22-OCT-2002; 2002WO-US033739.

PF

XX

XX 25-OCT-2001; 2001US-0337642P.

PR

XX

XX 09-JAN-2002; 2002US-0347694P.

PR

XX

XX (GETH) GENENTECH INC.

PA

XX

XX Presta LG;

PI

XX

XX WPI; 2003-421411/39.

DR

XX

XX New composition comprising a glycoprotein having a Fc region useful for

PT treating cancer, autoimmune disease, inflammatory disorder or infection

PT in a mammal.

PT

XX Disclosure; Fig 23; 139pp; English.

PS

XX The present sequence is the protein sequence of the Fc region of human

CC IgG4. A claimed composition comprises a glycoprotein having a Fc region.

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:49:37 ; Search time 18.0822 Seconds
(without alignments)
585.319 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLPPPKPDKT.....CKVSNKGLPSSIEKTIISKAK 110
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	327	1 G4HU	Ig gamma-4 chain C
2	542.5	93.1	326	1 G2HU	Ig gamma-2 chain C
3	541	92.8	234	2 PT0207	Ig gamma chain C r
4	541	92.8	255	4 S31866	Ig gamma-1 chain C
5	541	92.8	330	1 GHU	Ig gamma-1 chain C
6	541	92.8	374	2 S69339	Ig heavy chain V r
7	531	91.1	377	2 A23511	Ig gamma-3 chain C
8	531	91.1	377	2 A60764	Ig gamma-3 chain C
9	518	88.9	289	1 G3HUI	Ig gamma-3 heavy c
10	470	80.6	328	2 I47160	Ig gamma 2b chain
11	470	80.6	328	2 I47159	Ig gamma 2a chain
12	465	79.8	277	2 I47152	Ig gamma 4 chain c
13	443	76.0	328	2 I47161	Ig gamma 3 chain c
14	443	76.0	328	2 I47158	Ig gamma 1 chain c
15	433	74.3	308	2 C30554	Ig heavy chain C r
16	433	74.3	323	1 GHRB	Ig gamma chain C r
17	433	74.3	333	2 PS0018	Ig gamma-2b chain
18	433	74.3	472	2 S31459	Ig gamma-1 chain -
19	431	73.9	470	2 S22080	Ig heavy chain pre
20	426	73.1	329	1 G2GP	Ig gamma-2 chain C
21	417	71.5	329	1 G3MSC	Ig gamma-3 chain C
22	417	71.5	328	1 G3MSM	Ig gamma-3 chain C
23	409	70.2	327	2 S06611	Ig gamma-2 chain C
24	405	69.5	324	1 G1MS	Ig gamma-1 chain C
25	405	69.5	393	1 G1MSM	Ig gamma-1 chain C
26	405	69.5	444	2 PC4436	monoclonal antibod
27	403	69.1	329	2 S00847	Ig gamma-2c chain
28	399	68.4	405	1 G2MSBM	Ig gamma-2b chain
29	399	68.4	474	1 G2MS11	Ig gamma-2b chain

30	396	67.9	335	1 G2MSAB	Ig gamma-2a chain
31	393	67.4	330	1 G2MSA	Ig gamma-2a chain
32	393	67.4	399	1 G2MSGAM	Ig gamma-2a chain
33	393	67.4	469	2 S37483	Ig gamma-2a chain
34	389	66.7	326	2 PS0017	Ig gamma-1 chain C
35	385	66.0	475	2 S01321	Ig gamma-2b chain
36	383	65.7	446	2 S40295	Ig gamma-2a chain
37	343	58.8	322	2 PS0019	Ig gamma-2a chain
38	311	53.3	112	2 B30503	Ig gamma-2a chain
39	278	47.7	88	2 A30503	Ig gamma-2b chain
40	258	44.3	180	2 I46732	Ig gamma heavy cha
41	167.5	28.7	426	2 I36948	Ig epsilon-chain -
42	166.5	28.6	428	1 EHHU	Ig epsilon chain C
43	165	28.3	152	2 S14236	Ig gamma-1 chain C
44	154	26.4	549	2 S04845	Ig heavy chain pre
45	151	25.9	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin C region; immunoglobulin homology
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.9%; Score 565; DB 1; Length 327;
Best Local Similarity 97.3%; Pred. No. 6.3e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 APPVAGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYDVGVVHNATK 60
Db 111 ABEFLGPGSVFLPPPKDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYDVGVVHNATK 170
Qy 61 PREEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 171 PREEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 220

RESULT 2

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A9306; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain components
A:Reference number: A9306; MUID:82197621; PMID:6804948
A:Accession: A9306
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; EMBL:143233.33
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional studies
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Accession: A92809
A:Contents: myeloma protein T11
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 molecule
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-199
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G2
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidation of residue 268

Query Match

Best Local Similarity 93.1%; Score 542.5; DB 1; Length 326;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFQWYVDGVEVHNAKTK 60

DB 111 APPVA-GPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFQWYVDGVEVHNAKTK 169

QY 61 PREQFNSTYRVSVLTIVLHQLDNLNGKEYCKVSKNGLPSSIEKTIKAK 110

DB 170 PREQFNSTYRVSVLTIVLHQLDNLNGKEYCKVSKNGLPAPIEKTIKTK 219

RESULT 3

PT0207

Ig gamma chain C region - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999

C:Accession: PT0207

R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.

Mol. Immunol. 28, 319-322, 1991

A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.

A:Reference number: PT0207; MUID:91287716; PMID:2062315

A:Accession: PT0207

A:Molecule type: mRNA

A:Residues: 1-234 <EHR>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:48-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 92.8%; Score 541; DB 2; Length 234;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFQWYVDGVEVHNAKTK 60

DB 25 APFLGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFQWYVDGVEVHNAKTK 84

QY 61 PREQFNSTYRVSVLTIVLHQLDNLNGKEYCKVSKNGLPSSIEKTIKAK 110

DB 85 PREQFNSTYRVSVLTIVLHQLDNLNGKEYCKVSKNGLPAPIEKTIKTK 134

RESULT 4

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C:Accession: S31866

R:Filpula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products.

A:Reference number: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>

A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C:Keywords: immunoglobulin

F:1-22/Region: Escherichia coli outer membrane protein A precursor

F:23-255/Region: human Ig gamma-1 chain C region

Query Match

Best Local Similarity 92.8%; Score 541; DB 4; Length 255;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFQWYVDGVEVHNAKTK 60

DB 39 APFLGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFQWYVDGVEVHNAKTK 98

QY 61 PREQFNSTYRVSVLTIVLHQLDNLNGKEYCKVSKNGLPSSIEKTIKAK 110

DB 85 PREQFNSTYRVSVLTIVLHQLDNLNGKEYCKVSKNGLPAPIEKTIKTK 134

Db 99 PREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAK 148

RESULT 5

GHUU

Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C/Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146

R/Elison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; MUID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <ELL>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A/Note: Lys-330 is removed after translation

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A/Reference number: A90563; MUID:71064024; PMID:5489771

A/Contents: myeloma protein Eu

A/Accession: B90563

A/Molecule type: Protein

A/Residues: 1-96,'R',98-135 <CUN>

A/Note: this sequence has the G1m(3) marker, 97-Arg

R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A/Reference number: A90564; MUID:71064025; PMID:5530842

A/Contents: Eu

A/Accession: A90564

A/Molecule type: protein

A/Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A/Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R/Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A/Reference number: A91668; MUID:77070269; PMID:826475

A/Contents: myeloma protein Nie

A/Accession: B91668

A/Molecule type: protein

A/Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27

A/Note: this sequence has the G1m(17) and G1m(1) markers

R/Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A/Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI

A/Reference number: A91723; MUID:83289131; PMID:6884994

A/Contents: myeloma protein KOI; disulfide bonds

A/Accession: A91723

A/Molecule type: protein

A/Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH

A/Note: this sequence has the G1m(3) and G1m(non-1) markers

R/Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid

A/Reference number: A90565; MUID:71064027; PMID:4923144

A/Contents: annotation; disulfide bonds

R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

enbromide cleavage products, and the disulfide bridges

A/Reference number: A91667; MUID:77070267; PMID:11002129

A/Contents: annotation; disulfide bonds

C/Genetics:

A/Gene: IGHG1

A/Cross-references: GDB:120085; OMIM:147100

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1; 114/1; 224/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology <IM1>

F/137-206/Domain: immunoglobulin homology <IM2>

F/243-310/Domain: immunoglobulin homology <IM3>

F/27-83,144-204,250-308/Disulfide bonds: #status experimental

F/103/Disulfide bonds: interchain (to light chain) #status experimental

F/109,112/Disulfide bonds: interchain (to heavy chain) #status experimental

F/180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 92.8%; Score 541; DB 1; Length 330;

Best Local Similarity 91.8%; Pred. No. 1.6e-46;

Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60

Db 114 APBLLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 173

Qy 61 PREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTSKAK 110

Db 174 PREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPAPIEKTISKAK 223

RESULT 6

S69339

Ig heavy chain V region precursor - human

C/Species: Homo sapiens (man)

C/Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 01-Dec-2000

C/Accession: S69339; S72664

R/Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A/Reference number: S69339; MUID:95262687; PMID:7744049

A/Accession: S69339

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-374 <KHA>

A/Cross-references: EMBL:X81695

R/Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A/Reference number: S72664

A/Accession: S72664

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-140,'C',142-374 <KH2>

A/Cross-references: EMBL:X81695

C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 92.8%; Score 541; DB 2; Length 374;

Best Local Similarity 91.8%; Pred. No. 1.9e-46;

Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60

Db 158 APBLLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 217

Qy 61 PREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTSKAK 110

A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: mRNA
A;Residues: 1-277 <AC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 465; DB 2; Length 277;
Best Local Similarity 80.8%; Pred. No. 5.2e-39;
Matches 84; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 7 GPSVFIFPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVEVHNAKTKPRBEQF 66
||| ||:||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 65 GPFAFIFFPPPKPDTLMISRTPKVTCVVVDVSQENPEVQFSWYDGVGVEVHTAQTRPKBEQF 124

Qy 67 NSTYRVVSVLTVLHQDLWGKEYCKVKNSKGLPSSIEKTISKAK 110
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 125 NSTYRVVSVLPVLIHQDLWGKEFKCKNNKDLPAPIRILSKAK 168

RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacs Kovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: mRNA
A;Residues: 1-328 <XAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 443; DB 2; Length 328;
Best Local Similarity 78.6%; Pred. No. 1e-36;
Matches 81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 7 GPSVFIFPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVEVHNAKTKPRBEQF 66
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 116 GPSVFIFPPPKPDTLMISQTPEVTCTVVVDVSKGHAEEVQFSWYDGVGVEVHTAEIRPKBEQF 175

Qy 67 NSTYRVVSVLTVLHQDLWGKEYCKVKNSKGLPSSIEKTISKAK 109
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 176 NSTYRVVSVLPVLIHQDLWGKEFKCKNNVNDLPAPIRILSKAK 218

RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacs Kovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: mRNA
A;Residues: 1-328 <XAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IG1

C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 443; DB 2; Length 328;
Best Local Similarity 78.6%; Pred. No. 1e-36;
Matches 81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
116 GPSVFIPPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 175

QY 67 NSTYRVVSVLTVTLQDWLNQKEYKCKVSNKGLPSSIEKTIKSA 109
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
176 NSTYRVVSVLTPIQHDWLKQKFKPKCKVNNVDLPAPITRTISKA 218

RESULT 15

C30554
Ig heavy chain C region - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: C30554
R;Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:89093962; PMID:2492052
A;Accession: C30554
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-308 <FOL>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;113-182/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 433; DB 2; Length 308;
Best Local Similarity 71.6%; Pred. No. 9.4e-36;
Matches 78; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 2 PPVAGGVSFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
Db |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
91 PELPGGPSVFIFPPPKPKDTLTISGTEVTCVVVDVQDDPEVQFSFVNDVNEVTRTKP 150

QY 62 REQFNSTYRVSVLTVTLQDWLNQKEYKCKVSNKGLPSSIEKTIKSAK 110
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 REQFNSTYRVSGALPIQHQDWTGKGKFKCKVHNEALPAPIVRTISRTK 199

Search completed: November 17, 2005, 07:11:38
Job time : 19.0822 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 80.6164 Seconds
(without alignments)
698.725 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGPSVFLPPPKDKOT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	565	96.9	327	1	GC4_HUMAN	P01861 homo sapien
2	565	96.9	473	2	Q8TC63	Q8tc63 homo sapien
3	562	96.4	476	2	Q6MZX7	Q6mzx7 homo sapien
4	542.5	93.1	326	1	GC2_HUMAN	P01859 homo sapien
5	542.5	93.1	417	2	Q6N093	Q6n093 homo sapien
6	542.5	93.1	465	2	Q6P6C4	Q6p6c4 homo sapien
7	541	92.8	330	1	GC1_HUMAN	P01857 homo sapien
8	541	92.8	348	2	Q6PYX1	Q6pyx1 homo sapien
9	541	92.8	465	2	Q6GMX6	Q6gmx6 homo sapien
10	541	92.8	466	2	Q6IN78	Q6in78 homo sapien
11	541	92.8	469	2	Q7Z7P5	Q7z7p5 homo sapien
12	541	92.8	470	2	Q6PJ44	Q6pj44 homo sapien
13	541	92.8	470	2	Q7ZSW1	Q7zsw1 homo sapien
14	541	92.8	472	2	Q6N089	Q6n089 homo sapien
15	541	92.8	473	2	Q6MZV7	Q6mzv7 homo sapien
16	541	92.8	473	2	Q6P055	Q6p055 homo sapien
17	541	92.8	475	2	Q6GMW7	Q6gmw7 homo sapien
18	541	92.8	475	2	Q6MZQ6	Q6mzq6 homo sapien
19	541	92.8	475	2	Q6N095	Q6n095 homo sapien
20	541	92.8	476	2	Q6GMX1	Q6gmx1 homo sapien
21	541	92.8	478	2	Q6P181	Q6p181 homo sapien
22	541	92.8	480	2	Q6N094	Q6n094 homo sapien
23	541	92.8	480	2	Q6PJF1	Q6pjf1 homo sapien
24	541	92.8	481	2	Q6N097	Q6n097 homo sapien
25	541	92.8	482	2	Q7Z3S1	Q7z3s1 homo sapien
26	541	92.8	544	2	Q6PJ95	Q6pj95 homo sapien
27	541	92.8	679	2	Q96PQ8	Q96pq8 homo sapien
28	539.5	92.5	464	2	Q6MZU6	Q6mzu6 homo sapien
29	538	92.3	466	2	Q6N096	Q6n096 homo sapien
30	536	91.9	487	2	Q65ZL2	Q65zl2 mus sp. fv/
31	534	91.6	509	2	Q8NF17	Q8nf17 homo sapien

RESULT 1									
GC4_HUMAN									
ID	GC4_HUMAN	STANDARD;	PRT;	327	AA.				
AC	P01861;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	25-OCT-2004 (Rel. 45, Last annotation update)								
DE	IG gamma-4 chain C region.								
GN	Name=IGHG4;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=83157104; PubMed=6299662;								
RA	Ellison J.W., Buxbaum J.N., Hood L.E.;								
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";								
RL	DNA 1:11-18 (1981).								
RN	[2]								
RP	SEQUENCE OF 1-30 AND 81-326.								
RX	MEDLINE=70207560; PubMed=4192699;								
RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;								
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the								
RL	Biochem. J. 117:33-47 (1970).								
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; K01316; AAB59394.1; ALT_INIT.								
DR	PIR; A90933; G4HU.								
DR	PDB; 1AQD; X-ray; A=118-323.								
DR	Genew; HGNC:5528; IGHG4.								
DR	MIM; 147130; -								
DR	GO; GO:0005624; C:membrane fraction; NAS.								
DR	GO; GO:0003823; F:antigen binding; TAS.								
DR	GO; GO:0006955; P:immune response; NAS.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003597; Ig_c1.								
DR	InterPro; IPR003006; Ig_MHC.								
DR	Pfam; PF00047; ig; 3.								
DR	SMART; SM00407; IGC1; 2.								
DR	PROSITE; PS50835; IG_LIKE; 3.								
DR	PROSITE; PS00290; IG_MHC; 2.								
KW	3D-structure; Direct protein sequencing; Immunoglobulin C region;								
KW	Immunoglobulin domain.								
FT	NON_TER	1	98						
FT	DOMAIN	1	98	CHI.					

Q8n4y9 homo sapien
Q8ecn4 homo sapien
Q86ctt2 homo sapien
Q6n030 homo sapien
P01860 homo sapien
Q95m34 equus caball
P01870 oryctolagus
P20761 rattus norv
P01862 cavia porce
Q6kam2 mus musculu
P22436 mus musculu
P03987 mus musculu
Q7cmk1 mus musculu
P01868 mus musculu

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FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 96.9%; Score 565; DB 1; Length 327;
Best Local Similarity 97.3%; Pred. No. 3.9e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 111 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 170

QY 61 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 171 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 220

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 96.9%; Score 565; DB 2; Length 473;
Best Local Similarity 97.3%; Pred. No. 5.9e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 257 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 316

QY 61 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 317 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 366

RESULT 3
Q6MZK7 PRELIMINARY; PRT; 476 AA.
AC Q6MZK7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP6686M24218.
GN Name=DKFP6686M24218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; EX640824; CAE45900.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;

Query Match 96.4%; Score 562; DB 2; Length 476;
Best Local Similarity 96.4%; Pred. No. 1.2e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 260 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 319

QY 61 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 320 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 369

RESULT 4
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG gamma-2 chain C region.
GN Name=IGHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy
chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RA MEDLINE=83001943; PubMed=6329676;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RA MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequence of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulin gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulfide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;

RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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DR EMBL; J00230; AAB59393.1; -;
DR PIR; A93906; G2HU.
DR HSSP; P01857; 1OQX.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -;
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a heavy chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 103 103 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT VARIANT 60 60
FT CONFLICT 109 109 At or near the complement-binding site.
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
SQ
Query Match 93.1%; Score 542.5; DB 1; Length 326;
Best Local Similarity 93.6%; Pred. No. 6.9e-46;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Qy 1 APPVAGGVSFLFPKPKDTLMISRTPEVTCVVVDVSDPEQFVFNWYVDGVEVHNAKTK 60
Db 111 APVVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 169
Qy 61 PREEQNSTYRVVSVLTITLVHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 170 PREEQNSTFRVSVLTITLVHQLDNLNGKEYKCKVSNKGLPAPIETISKT 219
RESULT 5
Q6N093
ID Q6N093 PRELIMINARY; PRT; 417 AA.
AC Q6N093;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I04196 (Fragment).
GN Name=DKFZp686I04196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA The German Human cDNA Consortium;
RG Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CA845777.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518B844CFB883C CRC64;

Query Match 93.1%; Score 542.5; DB 2; Length 417;
Best Local Similarity 93.6%; Pred. No. 9.1e-46;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVVHNATK 60
Db 202 APPVA-GPSVFLPPPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVVHNATK 260
QY 61 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 261 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPAPIEKTSKTK 310

RESULT 6
Q6P6C4 PRELIMINARY; PRT; 465 AA.
ID Q6P6C4
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD99348ADC37E6D CRC64;

Query Match 93.1%; Score 542.5; DB 2; Length 465;
Best Local Similarity 93.6%; Pred. No. 1e-45;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVVHNATK 60
Db 250 APPVA-GPSVFLPPPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVVHNATK 308
QY 61 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 309 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPAPIEKTSKTK 358

RESULT 7
GC1_HUMAN STANDARD; PRT; 330 AA.
ID GC1_HUMAN
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
DE Name-IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Wexdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid covalence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
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RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
 RT peptides of the H-chain, alignment of the tryptic peptides and
 RT discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
 RP [5]
 RN
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=684994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
 RP [6]
 RN
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196 (1970).
 RP [7]
 RN
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
 RP [8]
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370 (1981).
 CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC G1M(3) marker and the G1M (non-1) markers.
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A93433; GHHU.
 DR PDB: 1AJ7; X-ray; H=1-103.
 DR PDB: 1DSB; X-ray; B/H=1-101.
 DR PDB: 1DS1; X-ray; H=1-101.
 DR PDB: 1D6V; X-ray; H=1-101.
 DR PDB: 1DN2; X-ray; A/B=120-326.
 DR PDB: 1E4K; X-ray; A/B=106-329.
 DR PDB: 1FCL; X-ray; A/B=106-329.
 DR PDB: 1FC2; X-ray; D=106-329.
 DR PDB: 1FCC; X-ray; A=121-326.
 DR PDB: 1H2H; X-ray; H/K=1-330.
 DR PDB: 1I7Z; X-ray; B/D=1-103.
 DR PDB: 1IIS; X-ray; A/B=107-330.
 DR PDB: 1IIX; X-ray; A/B=107-330.
 DR PDB: 1L6X; X-ray; A=120-326.
 DR PDB: 1OQX; X-ray; A/B=119-330.
 DR PDB: 1OQX; X-ray; A/B=119-330.

DR PDB: 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHL1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C-membrane fraction; NAS.
 DR GO; GO:0003823; F-antigen binding; TAS.
 DR GO; GO:0006955; P-immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW 3D-structure; Direct-protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT NON_TER 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 Hinge.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 Interchain (with light chain).
 FT DISULFID 109 109 Interchain (with heavy chain).
 FT DISULFID 112 112 Interchain (with heavy chain).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97 N-linked (GlcNAc...).
 FT VARIANT 239 239 K -> R (in G1M(3) marker).
 FT VARIANT 241 241 /FTid=VAR_003886.
 FT VARIANT 241 241 D -> E (in G1M(non-1) marker).
 FT VARIANT 241 241 /FTid=VAR_003887.
 FT VARIANT 241 241 L -> M (in G1M(non-1) marker).
 FT VARIANT 241 241 /FTid=VAR_003888.
 FT STRAND 23 24
 FT STRAND 26 33
 FT STRAND 38 38
 FT STRAND 41 41
 FT TURN 42 45
 FT TURN 48 49
 FT STRAND 50 52
 FT STRAND 57 58
 FT TURN 59 61
 FT STRAND 62 71
 FT HELIX 73 75
 FT TURN 76 78
 FT STRAND 82 87
 FT TURN 88 91
 FT STRAND 92 97
 FT TURN 102 103
 FT STRAND 122 126
 FT TURN 130 134
 FT TURN 136 137
 FT STRAND 141 149
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 167
 FT STRAND 171 172
 FT STRAND 176 177
 FT TURN 179 180
 FT STRAND 183 190
 FT STRAND 193 197
 FT TURN 198 199
 FT TURN 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT STRAND 232 242
 FT HELIX 238 242
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 FT STRAND 261 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284

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FT STRAND      287      296
FT HELIX        297      301
FT TURN         302      303
FT STRAND       306      311
FT TURN         313      314
FT HELIX        316      318
FT STRAND       319      324
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Query Match      92.8%; Score 541; DB 1; Length 330;
Best Local Similarity 91.8%; Pred. No. 9.9e-46;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
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Qy 61 PREEQFNSTYRVSVLTTLVHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 174 PREEQNSTYRVSVLTTLVHQLDNLNGKEYCKVSNKALPAPIETIKAK 223

RESULT 8
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AC Q6PYX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; AY570731; AAS88328.1; -.
RA HSP; P01857; 1A77.
RA GO; GO:0004872; F:receptor activity; IEA.
RA InterPro; IPR007110; Ig-like.
RA InterPro; IPR003597; Ig cl.
RA InterPro; IPR003006; Ig_MHC.
RA Pfam; PF07654; Cl-set; 3.
RA SMART; SM00407; IGcl; 3.
RA PROSITE; PSS0835; IG_LIKE; 3.
RA PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Receptor.
FT NON TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;

Query Match      92.8%; Score 541; DB 2; Length 348;
Best Local Similarity 91.8%; Pred. No. 1.1e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy 61 PREEQFNSTYRVSVLTTLVHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 192 PREEQNSTYRVSVLTTLVHQLDNLNGKEYCKVSNKALPAPIETIKAK 241

RESULT 9
Q6GMX6 ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Primary B-Cells;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC073766; AAH73766.1; -.
RA InterPro; IPR003599; Ig.
RA InterPro; IPR007110; Ig-like.
RA InterPro; IPR003597; Ig cl.
RA InterPro; IPR003006; Ig_MHC.
RA InterPro; IPR003596; Ig_v.
RA Pfam; PF07654; Cl-set; 3.
RA Pfam; PF00047; Ig; 4.
RA SMART; SM00409; IG; 2.
RA SMART; SM00407; IGcl; 3.
RA SMART; SM00406; IGv; 1.
RA PROSITE; PSS0835; IG_LIKE; 4.
RA PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      92.8%; Score 541; DB 2; Length 465;
Best Local Similarity 91.8%; Pred. No. 1.5e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
Db 249 APPELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 308

Qy 61 PREEQFNSTYRVSVLTTLVHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 309 PREEQNSTYRVSVLTTLVHQLDNLNGKEYCKVSNKALPAPIETIKAK 358

RESULT 10
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AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Search completed: November 17, 2005, 07:10:20
Job time : 80.6164 secs

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.6119 Seconds
(without alignments)
333.636 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLPPPKKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: Issued Patents AA:*
 - 2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 7: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	97.8	449	4	US-09-968-362A-20
2	565	96.9	110	3	US-08-444-644-44
3	565	96.9	110	3	US-08-232-246A-44
4	565	96.9	218	4	US-09-483-588-7
5	565	96.9	229	4	US-09-968-362A-28
6	565	96.9	327	2	US-08-761-277A-47
7	565	96.9	329	4	US-09-313-942-12
8	565	96.9	382	1	US-08-470-299-7
9	565	96.9	382	1	US-08-470-299-10
10	565	96.9	443	5	PCT-US96-13152-4
11	565	96.9	467	1	US-08-704-744-81
12	565	96.9	467	2	US-07-916-098A-45
13	565	96.9	467	3	US-08-523-894-8
14	565	96.9	467	3	US-08-523-894-10
15	565	96.9	467	3	US-08-523-894-12
16	561	96.2	109	2	US-08-070-116A-4
17	561	96.2	109	4	US-08-557-050-4
18	559	95.9	326	3	US-08-808-720-3
19	559	95.9	326	4	US-09-467-638-3
20	559	95.9	328	3	US-08-808-720-1
21	559	95.9	328	4	US-09-467-638-1
22	559	95.9	331	3	US-08-808-720-5
23	559	95.9	331	3	US-08-808-720-7
24	559	95.9	331	4	US-09-467-638-5
25	559	95.9	331	4	US-09-467-638-7
26	559	95.9	374	4	US-09-227-595-26
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28	559	95.9	374	4	US-08-595-590B-26	Sequence 26, Appl
29	559	95.9	374	4	US-08-595-590B-28	Sequence 28, Appl
30	554	95.0	447	4	US-09-968-362A-22	Sequence 22, Appl
31	547.5	93.9	448	4	US-09-968-362A-18	Sequence 18, Appl
32	546	93.7	468	3	US-09-485-737B-67	Sequence 67, Appl
33	546	93.7	468	4	US-10-071-485-67	Sequence 67, Appl
34	546	93.7	488	4	US-09-499-846-12	Sequence 12, Appl
35	546	93.7	497	4	US-09-499-846-10	Sequence 10, Appl
36	546	93.7	525	4	US-09-499-846-8	Sequence 8, Appl
37	546	93.7	711	3	US-09-485-737B-90	Sequence 90, Appl
38	546	93.7	711	4	US-10-071-485-90	Sequence 90, Appl
39	542.5	93.1	109	3	US-08-444-644-30	Sequence 30, Appl
40	542.5	93.1	109	3	US-08-232-246A-30	Sequence 30, Appl
41	542.5	93.1	217	4	US-09-483-588-5	Sequence 5, Appl
42	542.5	93.1	228	4	US-09-968-362A-27	Sequence 27, Appl
43	542.5	93.1	432	3	US-08-477-460B-2	Sequence 2, Appl
44	542.5	93.1	432	3	US-08-379-516-2	Sequence 2, Appl
45	542.5	93.1	432	3	US-09-329-916-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-968-362A-20
; Sequence 20, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 449
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: B)
US-09-968-362A-20

Query Match	97.8%	Score	570;	DB	4;	Length	449;
Best Local Similarity	98.2%	Pred. No.	2.2e-60;				
Matches	108;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;						
QY	1	APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK	60				
DB	233	APFEAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK	292				
QY	61	PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK	110				
DB	293	PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK	342				

RESULT 2
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Frideen, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-444-644-44

Query Match 96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
Db 1 APEFLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
QY 61 PREQFNSTYRVSVTLVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREQFNSTYRVSVTLVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAK 110

RESULT 3
US-08-232-246A-44
Sequence 44, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-232-246A-44

Query Match 96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
Db 1 APEFLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
QY 61 PREQFNSTYRVSVTLVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREQFNSTYRVSVTLVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAK 110

RESULT 4
US-09-483-588-7
Sequence 7, Application US/09483588
Patent No. 6737056
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
FILE REFERENCE: P1726R1
CURRENT APPLICATION NUMBER: US/09/483,588
CURRENT FILING DATE: 2000-01-14
EARLIER APPLICATION NUMBER: US 60/116,023
EARLIER FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
LENGTH: 218
TYPE: PRT
ORGANISM: homo sapiens
US-09-483-588-7

Query Match 96.9%; Score 565; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 3.4e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
Db 2 APEFLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 61
QY 61 PREQFNSTYRVSVTLVTLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAK 110

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Db 62 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 111
|||||
RESULT 5
US-09-968-362A-28
; Sequence 28, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Human IgG4 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-28

Query Match 96.9%; Score 565; DB 4; Length 229;
Best Local Similarity 97.3%; Pred. No. 3.6e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 13 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 72
Qy 61 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 110
Db 73 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 122

RESULT 6
US-08-761-277A-47
; Sequence 47, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOP-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
```

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; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-761-277A-47

Query Match 96.9%; Score 565; DB 2; Length 327;
Best Local Similarity 97.3%; Pred. No. 5.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 111 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170
Qy 61 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 110
Db 171 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 220

RESULT 7
US-09-313-942-12
; Sequence 12, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-12

Query Match 96.9%; Score 565; DB 4; Length 329;
Best Local Similarity 97.3%; Pred. No. 5.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 113 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 172
Qy 61 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 110
Db 173 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTISKAK 222

RESULT 8
US-08-470-299-7
; Sequence 7, Application US/08470299
; Patent No. 5783181
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael J.
; APPLICANT: Murphy, Kay E.
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Clinkenbeard, Helen E.
; APPLICANT: Young, Peter R.
; APPLICANT: Shatzman, Allan R.
; TITLE OF INVENTION: No. 5783181el Compounds
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
```

/ CITY: King of Prussia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19406
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,299
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sutton, Jeffrey A.
/ REGISTRATION NUMBER: 34,028
/ REFERENCE/DOCKET NUMBER: P31005C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5024
/ TELEFAX: 610-270-5090
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 382 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-470-299-7

Query Match 96.9%; Score 565; DB 1; Length 382;
Best Local Similarity 97.3%; Pred. No. 7.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 166 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225

QY 61 PREEQFNSTYRVSVLTVHLQDNLNKGKEYCKVSNKGLPSSIEKTIKAK 110
Db 226 PREEQFNSTYRVSVLTVHLQDNLNKGKEYCKVSNKGLPSSIEKTIKAK 275

RESULT 9
US-08-470-299-10
/ Sequence 10, Application US/08470299
/ Patent No. 5783181
/ GENERAL INFORMATION:
/ APPLICANT: Browne, Michael J.
/ APPLICANT: Murphy, Kay E.
/ APPLICANT: Chapman, Conrad G.
/ APPLICANT: Clinkenbeard, Helen E.
/ APPLICANT: Young, Peter R.
/ APPLICANT: Shatzman, Allan R.
/ TITLE OF INVENTION: No. 5783181el Compounds
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road, P.O. Box 1539
/ CITY: King of Prussia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19406
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,299
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sutton, Jeffrey A.
/ REGISTRATION NUMBER: 34,028

/ REFERENCE/DOCKET NUMBER: P31005C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5024
/ TELEFAX: 610-270-5090
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 382 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-470-299-10

Query Match 96.9%; Score 565; DB 1; Length 382;
Best Local Similarity 97.3%; Pred. No. 7.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 166 APEFEGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225

QY 61 PREEQFNSTYRVSVLTVHLQDNLNKGKEYCKVSNKGLPSSIEKTIKAK 110
Db 226 PREEQFNSTYRVSVLTVHLQDNLNKGKEYCKVSNKGLPSSIEKTIKAK 275

RESULT 10
PCT-US96-13152-4
/ Sequence 4, Application PC/TUS9613152
/ GENERAL INFORMATION:
/ APPLICANT: Martin, Ulrich, et al.
/ TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felte & Lynch
/ ADDRESSEE: Attn: Norman D. Hanson
/ STREET: 805 Third Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Computer Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/13152
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION NUMBER: 08/578,953
/ FILING DATE: 27-Dec-95
/ APPLICATION NUMBER: EP 95 112 895.8
/ FILING DATE: 17-Aug-95
/ APPLICATION NUMBER: EP 95 114 969.9
/ FILING DATE: 19-Sep-95
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Norman D. Hanson
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 443
/ TYPE: amino acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLESCULE TYPE: protein
/ PCT-US96-13152-4

Query Match 96.9%; Score 565; DB 5; Length 443;


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Best Local Similarity 97.3%; Pred. No. 8.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 227 APEFLGGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 286

QY 61 PREEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 287 PREEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 336

RESULT 11
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-704-744-81

Query Match 96.9%; Score 565; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 9.5e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 251 APEFLGGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

QY 61 PREEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 311 PREEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 360
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```
RESULT 12
US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-916-098A-45

Query Match 96.9%; Score 565; DB 2; Length 467;
Best Local Similarity 97.3%; Pred. No. 9.5e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 252 APEFLGGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 311

QY 61 PREEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 312 PREEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 361

RESULT 13
US-08-523-894-8
; Sequence 8, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
```

;/ TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;/ NUMBER OF SEQUENCES: 59
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;/ STREET: 699 Prince Street
;/ CITY: Alexandria
;/ STATE: VA
;/ COUNTRY: USA
;/ ZIP: 22314-3187
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/523,894
;/ FILING DATE: 06-SEP-1995
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Teskin, Robin L.
;/ REGISTRATION NUMBER: 35,030
;/ REFERENCE/DOCKET NUMBER: 012712-165
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 703-836-6620
;/ TELEFAX: 703-836-2021
;/ INFORMATION FOR SEQ ID NO: 8:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 467 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-523-894-8

Query Match 96.9%; Score 565; DB 3; Length 467;
Best Local Similarity 97.3%; Pred. No. 9.5e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 251 APEFLGGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310
QY 61 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYCKVSKNKGFLPSSIEKTISKAK 110
Db 311 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYCKVSKNKGFLPSSIEKTISKAK 360

RESULT 14
US-08-523-894-10
;/ Sequence 10, Application US/08523894
;/ Patent No. 6136310
;/ GENERAL INFORMATION:
;/ APPLICANT: Hanna, Nabil
;/ APPLICANT: Newman, Roland A.
;/ APPLICANT: Reff, Mitchell E.
;/ TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;/ TITLE OF INVENTION: Therapy
;/ NUMBER OF SEQUENCES: 59
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;/ STREET: 699 Prince Street
;/ CITY: Alexandria
;/ STATE: VA
;/ COUNTRY: USA
;/ ZIP: 22314-3187
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/523,894
;/ FILING DATE: 06-SEP-1995

;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Teskin, Robin L.
;/ REGISTRATION NUMBER: 35,030
;/ REFERENCE/DOCKET NUMBER: 012712-165
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 703-836-6620
;/ TELEFAX: 703-836-2021
;/ INFORMATION FOR SEQ ID NO: 10:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 467 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-523-894-10

Query Match 96.9%; Score 565; DB 3; Length 467;
Best Local Similarity 97.3%; Pred. No. 9.5e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 251 APEFLGGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310
QY 61 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYCKVSKNKGFLPSSIEKTISKAK 110
Db 311 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYCKVSKNKGFLPSSIEKTISKAK 360

RESULT 15
US-08-523-894-12
;/ Sequence 12, Application US/08523894
;/ Patent No. 6136310
;/ GENERAL INFORMATION:
;/ APPLICANT: Hanna, Nabil
;/ APPLICANT: Newman, Roland A.
;/ APPLICANT: Reff, Mitchell E.
;/ TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;/ TITLE OF INVENTION: Therapy
;/ NUMBER OF SEQUENCES: 59
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;/ STREET: 699 Prince Street
;/ CITY: Alexandria
;/ STATE: VA
;/ COUNTRY: USA
;/ ZIP: 22314-3187
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/523,894
;/ FILING DATE: 06-SEP-1995
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Teskin, Robin L.
;/ REGISTRATION NUMBER: 35,030
;/ REFERENCE/DOCKET NUMBER: 012712-165
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 703-836-6620
;/ TELEFAX: 703-836-2021
;/ INFORMATION FOR SEQ ID NO: 12:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 467 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-523-894-12

Query Match 96.9%; Score 565; DB 3; Length 467;
Best Local Similarity 97.3%; Pred. No. 9.5e-60;

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Db	251	APEFEGGSPV	ELFP	PKPKDTLMISRTPEVTCVVVDV	SVQEDPEVFQFNWYVDGVEVHNA	TK	310			
Qy	61	PREEQFNSTY	RVVSVLTVL	HQDWLN	NGKEYCKVSNKGLPSSIE	KTISKAK	110			
Db	311	PREEQFNSTY	RVVSVLTVL	HQDWLN	NGKEYCKVSNKGLPSSIE	KTISKAK	360			

Search completed: November 17, 2005, 07:13:22
Job time : 24.6119 secs

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GenCore version 5.1.6.
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 84.3836 Seconds
(without alignments)
545.427 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583

Sequence: 1 APPVAGGPSVFLPPPKPKDT.....CKVSNKGLPSSIKTISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	576	98.8	110	18	US-10-959-318-9
2	573	98.3	110	18	US-10-959-318-10
3	571	97.9	110	20	US-11-018-102-25
4	570	97.8	437	10	US-09-932-812-20
5	570	97.8	437	16	US-10-761-593A-20
6	570	97.8	437	20	US-11-016-518A-20
7	570	97.8	437	20	US-11-017-185-20
8	570	97.8	449	10	US-09-968-362-20
9	570	97.8	449	16	US-10-800-497-20
10	570	97.8	449	16	US-10-800-449-20
11	566.5	97.2	442	14	US-10-006-593-67
Sequence 9, Appl1					
Sequence 10, Appl					
Sequence 25, Appl					
Sequence 20, Appl					
Sequence 20, Appl					
Sequence 20, Appl					
Sequence 20, Appl					
Sequence 20, Appl					
Sequence 20, Appl					
Sequence 20, Appl					

12	566.5	97.2	472	15	US-10-307-724-67	Sequence 67, Appl
13	566.5	97.2	472	16	US-10-737-290-67	Sequence 67, Appl
14	565	96.9	110	18	US-10-959-318-4	Sequence 4, Appl1
15	565	96.9	110	20	US-11-018-102-24	Sequence 24, Appl
16	565	96.9	218	9	US-09-813-341-5	Sequence 5, Appl1
17	565	96.9	218	14	US-10-277-370-5	Sequence 5, Appl1
18	565	96.9	218	14	US-10-196-394-76	Sequence 76, Appl
19	565	96.9	218	15	US-10-370-749-18	Sequence 18, Appl
20	565	96.9	218	16	US-10-835-642-7	Sequence 7, Appl1
21	565	96.9	218	16	US-10-757-863-7	Sequence 7, Appl1
22	565	96.9	218	17	US-10-982-470-7	Sequence 7, Appl1
23	565	96.9	218	17	US-11-158-839-7	Sequence 7, Appl1
24	565	96.9	219	16	US-10-704-406-6	Sequence 6, Appl1
25	565	96.9	229	16	US-10-761-593A-28	Sequence 28, Appl
26	565	96.9	229	16	US-10-800-497-28	Sequence 28, Appl
27	565	96.9	229	16	US-10-800-449-28	Sequence 28, Appl
28	565	96.9	229	20	US-11-016-518A-28	Sequence 28, Appl
29	565	96.9	229	20	US-11-017-185-28	Sequence 28, Appl
30	565	96.9	266	18	US-10-609-783B-51	Sequence 51, Appl
31	565	96.9	284	15	US-10-433-108-24	Sequence 24, Appl
32	565	96.9	327	9	US-09-925-664-47	Sequence 47, Appl
33	565	96.9	327	11	US-09-925-192-47	Sequence 47, Appl
34	565	96.9	327	13	US-10-047-542-26	Sequence 26, Appl
35	565	96.9	327	14	US-10-310-719-7	Sequence 7, Appl1
36	565	96.9	327	14	US-10-112-582-4	Sequence 4, Appl1
37	565	96.9	327	15	US-10-656-769-8	Sequence 8, Appl1
38	565	96.9	327	17	US-10-822-300-114	Sequence 114, App
39	565	96.9	327	17	US-10-822-300-116	Sequence 116, App
40	565	96.9	327	17	US-10-872-932A-39	Sequence 39, Appl
41	565	96.9	327	17	US-10-891-972-171	Sequence 171, App
42	565	96.9	327	17	US-10-928-305-6	Sequence 6, Appl1
43	565	96.9	327	17	US-10-891-658-6	Sequence 6, Appl1
44	565	96.9	327	17	US-10-982-359-77	Sequence 77, Appl
45	565	96.9	327	17	US-10-937-596-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215788A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)
US-10-959-318-9

Query Match 98.8%; Score 576; DB 18; Length 110;
Best Local Similarity 98.2%; Pred. No. 3.9e-48;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRPETVCVVVDVSQEDPEVFNWYVDGVEVHNATK 60
Db 1 APPVAGGPSVFLPPPKPKDTLMISRPETVCVVVDVSQEDPEVFNWYVDGVEVHNATK 60

Qy	61	PREOFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTI	110
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Db	61	PREOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTI	110

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RESULT 2
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and e (5268)
US-10-959-318-10

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RESULT 3
US-11-018-102-25
; Sequence 25, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018,102
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: engineered G4 CH2
US-11-018-102-25

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Db
61 PREEFNSTYRVSVLTVLHODWLNNGKEYCKVSNKGLPSSIEKTSKAK 110

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RESULT 4
US-09-932-812-20
; Sequence 20, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of
; FILE REFERENCE: 025UN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-VFC gamma4 wi
; OTHER INFORMATION: }
US-09-932-812-20

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RESULT 5
US-10-761-593A-20
; Sequence 20, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure
; OTHER INFORMATION: 2B)
US-10-761-593A-20

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Query Match 97.8%; Score 570; DB 16; Length 437;
Best Local Similarity 98.2%; Pred. No. 7.2e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110
Db 281 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 330

RESULT 6
US-11-016-518A-20
; Sequence 20, Application US/11016518A
; Publication No. US20050124045A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
; TITLE OF INVENTION: biological activities
; FILE REFERENCE: 02SUN2004D1
; CURRENT APPLICATION NUMBER: US/11/016.518A
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US 09/932,812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure
US-11-016-518A-20

Query Match 97.8%; Score 570; DB 20; Length 437;
Best Local Similarity 98.2%; Pred. No. 7.2e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60
Db 221 APEFAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 280

Qy 61 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110
Db 281 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 330

RESULT 7
US-11-017-185-20
; Sequence 20, Application US/11017185
; Publication No. US20050142642A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolog
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001D2
; CURRENT APPLICATION NUMBER: US/11/017.185
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US 09/932,812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2B
US-11-017-185-20

Query Match 97.8%; Score 570; DB 20; Length 437;
Best Local Similarity 98.2%; Pred. No. 7.2e-47;
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Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60
Db 221 APEFAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 280

Qy 61 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110
Db 281 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 330

RESULT 8
US-09-968-362-20
; Sequence 20, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968.362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2
US-09-968-362-20

Query Match 97.8%; Score 570; DB 10; Length 449;
Best Local Similarity 98.2%; Pred. No. 7.4e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60
Db 233 APEFAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 292

Qy 61 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110
Db 293 PREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 342

RESULT 9
US-10-800-497-20
; Sequence 20, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; TITLE OF INVENTION: stimulating factor with
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800.497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968.362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide
; OTHER INFORMATION: (Figure 2
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; OTHER INFORMATION: B)
US-10-800-497-20

Query Match          97.8%; Score 570; DB 16; Length 449;
Best Local Similarity 98.2%; Pred. No. 7.4e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 233 APEFAGGPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 292

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 293 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 342

RESULT 10
US-10-800-449-20
; Sequence 20, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: B)
US-10-800-449-20

Query Match          97.8%; Score 570; DB 16; Length 449;
Best Local Similarity 98.2%; Pred. No. 7.4e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 233 APEFAGGPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 292

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 293 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 342

RESULT 11
US-10-006-593-67
; Sequence 67, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67
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; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67

Query Match          97.2%; Score 566.5; DB 14; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.7e-46;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 257 APPVA-GPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 315

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 316 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 12
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2cid
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

Query Match          97.2%; Score 566.5; DB 15; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.7e-46;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 257 APPVA-GPSVFLPPPKDTLMSRTPETCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 315

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 316 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 13
US-10-737-290-67
; Sequence 67, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
```


APPLICANT: Renshaw, Mark
APPLICANT: Orenclia, Cecilia
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2 CIP III
CURRENT APPLICATION NUMBER: US/10/737,290
CURRENT FILING DATE: 2003-12-15
PRIORITY APPLICATION NUMBER: US 10/452,590
PRIORITY FILING DATE: 2003-06-02
PRIORITY APPLICATION NUMBER: US 10/307,724
PRIORITY FILING DATE: 2002-12-02
PRIORITY APPLICATION NUMBER: US 10/006,593
PRIORITY FILING DATE: 2001-12-05
PRIORITY APPLICATION NUMBER: US 60/251,448
PRIORITY FILING DATE: 2000-12-05
PRIORITY APPLICATION NUMBER: US 60/289,889
PRIORITY FILING DATE: 2001-05-04
PRIORITY APPLICATION NUMBER: US 60/294,068
PRIORITY FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 193
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67
LENGTH: 472
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Humanized antibody heavy chain
US-10-737-290-67

Query Match 97.2%; Score 566.5; DB 16; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.7e-46;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 257 APPVA-GPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315
Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 316 PREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 365

RESULT 14
US-10-959-318-4
Sequence 4, Application US/10959318
Publication No. US20050215768A1
GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIORITY APPLICATION NUMBER: PCT/GB2004/004254
PRIORITY FILING DATE: 2004-10-07
PRIORITY APPLICATION NUMBER: GB0324368.0
PRIORITY FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-10-959-318-4

Query Match 96.9%; Score 565; DB 18; Length 110;
Best Local Similarity 97.3%; Pred. No. 4.6e-47;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

Db 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
RESULT 15
US-11-018-102-24
Sequence 24, Application US/11018102
Publication No. US20050136061A1
GENERAL INFORMATION:
APPLICANT: Centocor, Inc.
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN5045 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-11-018-102-24

Query Match 96.9%; Score 565; DB 20; Length 110;
Best Local Similarity 97.3%; Pred. No. 4.6e-47;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

Search completed: November 17, 2005, 07:37:37
Job time : 85.3836 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.9087 Seconds
(without alignments)
473.187 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 593
Sequence: 1 APPVAGGPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	110	2	AAR41717 Undefined
2	561	96.2	109	2	AAR67438 Aar67438 OKT3 mono
3	560	96.1	110	3	AAY54998 Aay54998 Mutated C
4	554.5	95.1	109	3	AAY54996 Aay54996 Mutated C
5	542.5	93.1	109	2	AAR41709 Aar41709 Undefined
6	542.5	93.1	109	3	AAY54997 Aay54997 Mutated C
7	541	92.8	110	2	AAR27680 Aar27680 Human imm
8	541	92.8	110	2	AAR41684 Aar41684 Undefined
9	541	92.8	110	8	ADH75385 Adh75385 Human IgG
10	538	92.3	102	8	ADJ52132 Adj52132 CH1 delet
11	537	92.1	109	7	ADD25659 Add25659 Binding d
12	536	91.9	109	5	AAE28089 Aae28089 Human imm
13	536	91.9	110	8	ADH75415 Adh75415 CH2 regio
14	535	91.8	110	8	ADL90103 Adl90103 Human imm
15	534	91.6	110	8	ADH75413 Adh75413 CH2 regio
16	529	90.7	109	7	ADD25761 Add25761 Binding d
17	525	90.1	105	2	AAY42626 Aay42626 Human IgG
18	525	90.1	110	2	AAR41713 Aar41713 Undefined
19	512	87.8	102	8	ADJ52129 Adj52129 CH1 delet
20	414	71.0	110	2	AAW71023 Aaw71023 Mus muscu
21	399	68.4	110	1	AAP83207 Aap83207 Sequence
22	369	63.3	72	8	ADL15711 Adl15711 Human imm
23	328	56.3	66	2	AAR75349 Aar75349 C-gamma-1
24	328	56.3	66	2	AAR75351 Aar75351 C-gamma-1
25	327	56.1	76	8	ADL15713 Adl15713 Human imm

26	282	48.4	56	1	AAP83204 Aap83204 Sequence
27	277	47.5	56	1	AAP83201 Aap83201 Sequence
28	277	47.5	56	1	AAP83203 Aap83203 Sequence
29	276	47.3	56	1	AAP83202 Aap83202 Sequence
30	271	46.5	56	1	AAP83206 Aap83206 Sequence
31	271	46.5	56	1	AAP83205 Aap83205 Sequence
32	233	40.0	46	8	ADR59139 Adr59139 Human IgG
33	233	40.0	46	8	ADR59138 Adr59138 Human IgG
34	232.5	39.9	110	2	AAR33315 Aar33315 Variant I
35	227	38.9	46	8	ADR59143 Adr59143 Rhesus mo
36	225	38.6	46	8	ADR59142 Adr59142 Rhesus mo
37	206	35.3	46	8	ADR59140 Adr59140 Rhesus mo
38	206	35.3	46	8	ADR59141 Adr59141 Crab-eati
39	206	35.3	46	8	ADR59145 Adr59145 Pig IgG2a
40	206	35.3	46	8	ADR59148 Adr59148 Camel IgG
41	203	34.8	96	3	AAB53640 Aab53640 Human col
42	201.5	34.6	110	2	AAR33316 Aar33316 Variant I
43	199	34.1	50	8	ADR59144 Adr59144 Optimum I
44	196	33.6	46	8	ADR59147 Adr59147 Llama IgG
45	196	33.6	46	8	ADR59152 Adr59152 Bovine Ig

ALIGNMENTS

RESULT 1
AAR41717
ID AAR41717 standard; protein; 110 AA.
XX
AC AAR41717;
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
DE Undefined ORF2 encoded by plasmid pAH4808.
XX
KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
OS Synthetic.
XX
PN WO9310819-A1.
XX
PD 10-JUN-1993.
XX
PF 24-NOV-1992; 92WO-US010206.
XX
PR 26-NOV-1991; 91US-00800458.
XX
PA (ALKE-) ALKERMES INC.
XX
PI Friden PM;
XX
DR WPI; 1993-196742/24.
DR N-PSDB; AAQ43848.
XX
PT Antibody conjugates specific for transferrin receptor - used for
diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
PS Disclosure; Fig 19J; 151pp; English.
XX
CC The sequences given in AAR41715-18 are encoded by the expression vector
pAH4808. This vector represents the cloning of the human gamma isotype,
gamma-4, with the variable region of the murine monoclonal antibody
128.1. This plasmid encodes a chimeric monoclonal antibody in which the
heavy chain (VH) is derived from a murine source and the sequences
encoding CH1, CH2 and CH3 are derived from a human source. This vector,
in combination with the chimeric light chain vector, pAQ4611 (see also
AAQ43845), was transfected into SP2/0 cells and clones were isolated.

CC 128.1 is an anti-human transferrin receptor antibody which binds to the
 CC transferrin receptor on brain capillary endothelial cells. This antibody
 CC may be used in a conjugate in which it is linked to a neuropharmaceutical
 CC or diagnostic agent. The conjugate may be used to treat or prevent
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 110 AA;

Query Match 96.9%; Score 565; DB 2; Length 110;
 Best Local Similarity 97.3%; Pred. No. 4.9e-49;
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
 DB 1 APFELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
 QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 DB 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 2
 AAR67438
 ID AAR67438 standard; protein; 109 AA.
 XX AAR67438;
 AC AAR67438;
 DT 25-MAR-2003 (revised)
 DT 08-JUL-1995 (first entry)
 XX
 XX OKT3 monoclonal antibody fragment.
 XX
 KW OKT3; monoclonal antibody; antibody engineering; immunosuppressive;
 KW humanized antibody.
 XX
 OS Mus musculus.
 XX
 PN WO9428027-A1.
 XX
 PD 08-DEC-1994.
 XX
 XX 01-JUN-1994; 94WO-US006198.
 XX
 XX 01-JUN-1993; 93US-00070116.
 XX
 XX (ARCH-) ARCH DEV CORP.
 XX
 XX Bluestone JA, Zivin RA, Jolliffe L;
 XX
 XX WPI; 1995-022721/03.
 DR P-PSDB; AAQ75356.
 DR

XX New humanised OKT3 antibody with mutated Fc receptor binding region -
 PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
 PT cell activating side effects of wild type antibody.
 XX
 XX Disclosure; Page 82-87; 135pp; English.
 PS

XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-
 CC cell activating and immunosuppressive activity, and is used to treat
 CC transplant patients to prevent rejection. The antibody can be engineered
 CC to contain a human Fc region. By transferring the binding specificity
 CC into a human framework, the immunogenicity is reduced without affecting
 CC the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 109 AA;

Query Match 96.2%; Score 561; DB 2; Length 109;
 Best Local Similarity 97.2%; Pred. No. 1.2e-48;
 Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
 DB 1 PEFELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60
 QY 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 DB 61 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 3
 AAY54998
 ID AAY54998 standard; protein; 110 AA.
 XX AAY54998;
 AC AAY54998;
 DT 17-FEB-2000 (first entry)
 XX

XX Mutated CH2 sequence G1deltaaac.
 XX
 XX Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; Igg heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
 KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.
 XX
 OS Synthetic.
 XX
 PN WO9558572-A1.
 XX

PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-GB001441.
 XX
 PR 08-MAY-1998; 98GB-00009951.
 XX
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 PA
 XX Armour KL, Clark MR, Williamson LM;
 XX
 XX WPI; 2000-039075/03.
 DR

XX Immunoglobulin-derived binding molecules that do not activate complement
 PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
 PT properties.
 XX
 XX Claim 12; Fig 17; 81pp; English.
 PS

XX This sequence represents the mutated CH2 molecule G1deltaaac, and is a
 CC binding molecule of the invention. The recombinant binding molecule is
 CC capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcgammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of graft-vs-
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaRIIb and desirable
 CC IgG properties have been retained. The polypeptides do not contain non-

CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)

SQ Sequence 110 AA;

Query Match 96.1%; Score 560; DB 3; Length 110;
 Best Local Similarity 96.4%; Pred. No. 1.6e-48;
 Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLPPPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNATK 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 1 APPVAGGSPVFLPPPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNATK 60

OY 61 PREEQFNSTYRVSVSLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

DB 61 PREEQFNSTYRVSVSLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110

RESULT 4

AAY54996
 ID AAY54996 standard; protein; 109 AA.

XX AAY54996;

DT 17-FEB-2000 (first entry)

DE Mutated CH2 sequence Gideltaab.

XX Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
 KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; rheumatoid arthritis; Goodpastures disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.

XX Synthetic.

XX WO9958572-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001441.

XX 08-MAY-1998; 98GB-00009951.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Armour KL, Clark MR, Williamson LM;

XX WPI; 2000-039075/03.

XX Immunoglobulin-derived binding molecules that do not activate complement
 PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
 PT properties.

XX Claim 12; Fig 17; 81pp; English.

XX This sequence represents the mutated CH2 molecule Gideltaab, and is a
 CC binding molecule of the invention. The recombinant binding molecule is
 CC capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcgammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target

CC molecule. The binding molecule is useful for the treatment of graft-vs-
 CC host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.
 CC fetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain non-
 CC human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor)

SQ Sequence 109 AA;

Query Match 95.1%; Score 554.5; DB 3; Length 109;
 Best Local Similarity 96.4%; Pred. No. 5.5e-48;
 Matches 106; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 APPVAGGSPVFLPPPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNATK 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

DB 1 APPVA-GPSVFLPPPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNATK 59
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 PREEQFNSTYRVSVSLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

DB 60 PREEQFNSTYRVSVSLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 109

RESULT 5

AAR41709

ID AAR41709 standard; protein; 109 AA.

XX AAR41709;

XX 25-MAR-2003 (revised)

DT 20-OCT-1993 (first entry)

DE Undefined ORF2 encoded by plasmid pAH4625.

XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
 KW light; chain; variable; constant; region; anti-human; pAH4807;
 KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
 KW endothelial cell; conjugate; neuropharmacological; gamma-3; gamma-4;
 KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
 KW Parkinsons disease; Alzheimers disease; SP2/0 cell.

XX Synthetic.

XX WO9310819-A1.

XX 10-JUN-1993.

XX 24-NOV-1992; 92WO-US010206.

XX 26-NOV-1991; 91US-00800458.

XX (ALKE-) ALKERMES INC.

XX Friden PM;

XX WPI; 1993-196742/24.

XX N-PSDB; AAQ43846.

XX Antibody conjugates specific for transferrin receptor - used for
 PT diagnosis and treatment of cancer, AIDS and neurological disorders.

PS Disclosure; Fig 17J; 151pp; English.

XX The sequences given in AAR41707-09 are encoded by the expression vector
 CC pAH4625. This vector represents the cloning of the human gamma isotype,
 CC gamma-2, with the variable region of the murine monoclonal antibody

128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AA043845), was transfected into sp2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)

Query Match 93.1%; Score 542.5; DB 2; Length 109;
Best Local Similarity 93.6%; Pred. No. 8.9e-47;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVAGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 APPVA-GPSVFLFPFKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 59
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 PREQFNSTRVWSVLTVLHODWLNQKEYKCKVSKNKGILPSSIEKTIISKAK 110
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 PREQFNSTRVWSVLTVHODWLNQKEYKCKVSKNKGILPPIETISKTK 109
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
AA54997
ID AA54997 standard; protein; 109 AA.
XX
AC AA54997;
XX
DT 17-FEB-2000 (first entry)
XX
DE Mutated CH2 sequence Gdeltaa.
XX
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
OS Synthetic.
OS
PN WO9958572-A1.
XX
XX
PD 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB001441.
XX
XX 08-MAY-1998; 98GB-00009951.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Armour KL, Clark MR, Williamson LM;
PI
XX
XX WPI; 2000-039075/03.
XX
XX Immunoglobulin-derived binding molecules that do not activate complement
or trigger cytotoxic activities and maintaining desirable immunoglobulin
properties.
XX
XX Claim 12; Fig 17; 81pp; English.
XX
XX This sequence represents the mutated CH2 molecule G2deltaa, and is a
binding molecule of the invention. The recombinant binding molecule is
capable of binding a target molecule without triggering complement
activation.

CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC segdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.

XX Sequence 109 AA;

Query Match 92.1%; Score 537; DB 7; Length 109;
Best Local Similarity 91.7%; Pred. No. 3.2e-46;
Matches 100; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 PPVAGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEQFVFNWYVDGVGVHNAKTK 61
DB 1 PELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTK 60
QY 62 REEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSKNGLPSSIEKTIISKAK 110
DB 61 REEQNSTYRVSVSVLTVLHQLDMLNGKEYCKVSKNGLPSSIEKTIISKAK 109

RESULT 12

AAE28089
ID AAE28089 standard; protein; 109 AA.

XX AAE28089;

XX 13-DEC-2002 (first entry)

XX Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.

XX Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
XX vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
XX immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
XX anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
XX virucide.

XX Homo sapiens.

XX WO200260919-A2.

XX 08-AUG-2002.

XX 12-DEC-2001; 2001WO-US048432.

XX 12-DEC-2000; 2000US-0254884P.

XX 09-MAY-2001; 2001US-02899760P.

XX PA

(MED1-) MEDIMMUNE INC.

XX Dall'acqua W, Johnson LS, Ward ES;

XX WPI; 2002-666925/71.

XX Modified immunoglobulins useful in the treatment of autoimmune diseases,
XX comprises at least one amino acid modification relative to a wild-type
XX immunoglobulin constant domain.

XX Disclosure; Page 138; 147pp; English.

XX The invention relates to a modified immunoglobulin (IgG1) which comprises
XX an IGH constant domain having at least one amino acid modification. The
XX immunoglobulins are used in the treatment or prevention of a disease or
XX disorder by passive immunotherapy for vaccinating a subject and for in
XX vivo diagnosis of a subject. The disease and disorders include a gamma
XX globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
XX host, lymphoid malignancies and passive immunotherapies and also for the
XX treatment of various systemic infections. The present sequence is human
XX immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain

XX Sequence 109 AA;

Query Match 91.9%; Score 536; DB 5; Length 109;
Best Local Similarity 91.7%; Pred. No. 4e-46;
Matches 100; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEQFVFNWYVDGVGVHNAKTK 60
DB 1 APPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTK 60

QY 61 PREEQFNSTYRVSVSVLTVLHQLDMLNGKEYCKVSKNGLPSSIEKTIISKAK 109

DB 61 PREEQNSTYRVSVSVLTVLHQLDMLNGKEYCKVSKNGLPSSIEKTIISKAK 109

RESULT 13

ADH75415
ID ADH75415 standard; protein; 110 AA.

XX AC ADH75415;

XX 22-APR-2004 (first entry)

XX CH2 region K290S variant.

XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
XX autoimmune disease.

XX Unidentified.

XX US2004002587-A1.

XX 01-JAN-2004.

XX 20-FEB-2003; 2003US-00370749.

XX 20-FEB-2002; 2002US-0358161P.

XX (WATK/) WATKINS J D.

XX (ALLA/) ALLAN B.

XX Watkins JD, Allan B;

XX WPI; 2004-070755/07.

XX New composition comprising a variant of a parent polypeptide having at
XX least a portion of a Fe region, useful in treating e.g., autoimmune
XX diseases.

XX Disclosure; SEQ ID NO 53; 62pp; English.

XX The invention relates to a new composition comprising a variant of a
CC parent polypeptide having at least a portion of a Fc region. The variant
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
CC presence of effector cells more effectively than the parent polypeptide
CC and comprises at least one amino acid modification at position 280 in the
CC Fc region. The composition is useful in treating diseases e.g.,
CC autoimmune diseases. The present sequence represents a CH2 region
CC variant.
XX
SQ Sequence 110 AA;

Query Match 91.9%; Score 536; DB 8; Length 110;
Best Local Similarity 90.9%; Pred. No. 4.1e-46;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| : |||||
DB 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTS 60
|| : |||||
QY 61 PREQFNSTYRVVSVLTVTLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 110
||||:|||||
DB 61 PREQFNSTYRVVSVLTVTLHQLDMLNGKEYCKVSNKALPAPIEKTSKAK 110
||||:|||||

RESULT 14
ADL90103
ID ADL90103 standard; protein; 110 AA.
XX
AC ADL90103;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human immunoglobulin CH2 region, SEQ ID 2.
XX
XX Immune response; immunoglobulin; Ig; CH2 region; human.
XX
XX Homo sapiens.
XX
XX WO2004027049-A2.
XX
XX 01-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US030188.
XX
XX 20-SEP-2002; 2002US-0412219P.
XX
XX 14-MAR-2003; 2003WO-US007995.
XX
XX (ASTR-) ASTRAL INC.
XX
XX Bot A, Wang L, Smith D, Phillips B;
XX
XX WPI; 2004-295415/27.
XX
XX Generating an immune response to an antigen, useful for generating
PT desired T cell responses comprising administering an immunoglobulin having
PT one peptide epitope of the antigen attached to the immunoglobulin.
XX
XX Disclosure; Page 11; 154pp; English.
XX

The present invention relates to a method for generating an immune
CC response to an antigen in a patient. The method comprises administering
CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
CC least one peptide epitope of the antigen attached to the Ig or its
CC portion and administering the immunoglobulin or its portion in
CC conjunction with a RNA segment. A recombinant human Ig molecule capable
CC of binding to an Fc gamma receptor (FcγMAR) of an antigen presenting
CC cell (APC) was used to illustrate the invention. The recombinant human Ig
CC molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a
CC hinge region (ADL90104) and a flanking peptide (ADL90105).
XX
SQ Sequence 110 AA;

Query Match 91.8%; Score 535; DB 8; Length 110;
Best Local Similarity 90.9%; Pred. No. 5.1e-46;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| : |||||
DB 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
QY 61 PREQFNSTYRVVSVLTVTLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 110
||||:|||||
DB 61 PREQFNSTYRVVSVLTVTLHQLDMLNGKEYCKVSNKALPAPIEKTSKAK 110
||||:|||||

RESULT 15
ADH75413
ID ADH75413 standard; protein; 110 AA.
XX
AC ADH75413;
XX
XX 22-APR-2004 (first entry)
XX
XX CH2 region D280H variant.
XX
XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;
XX autoimmune disease.
XX
XX Unidentified.
XX
XX US2004002587-A1.
XX
XX 01-JAN-2004.
XX
XX 20-FEB-2003; 2003US-00370749.
XX
XX 20-FEB-2002; 2002US-0358161P.
XX
XX (WATK/) WATKINS J D.
XX (ALLA/) ALLAN B.
XX
XX Watkins JD, Allan B;
XX
XX WPI; 2004-070755/07.
XX
XX New composition comprising a variant of a parent polypeptide having at
PT least a portion of a Fe region, useful in treating e.g., autoimmune
PT diseases.
XX
XX Disclosure; SEQ ID NO 51; 62pp; English.
XX

The invention relates to a new composition comprising a variant of a
CC parent polypeptide having at least a portion of a Fc region. The variant
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the
CC presence of effector cells more effectively than the parent polypeptide
CC and comprises at least one amino acid modification at position 280 in the
CC Fc region. The composition is useful in treating diseases e.g.,
CC autoimmune diseases. The present sequence represents a CH2 region
CC variant.
XX
SQ Sequence 110 AA;

Query Match 91.6%; Score 534; DB 8; Length 110;
Best Local Similarity 90.9%; Pred. No. 6.5e-46;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| : |||||
DB 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
QY 61 PREQFNSTYRVVSVLTVTLHQLDMLNGKEYCKVSNKGLPSSIEKTSKAK 110
||||:|||||
DB 61 PREQFNSTYRVVSVLTVTLHQLDMLNGKEYCKVSNKALPAPIEKTSKAK 110
||||:|||||

Search completed: November 17, 2005, 07:47:01
Job time : 90.9087 secs

11/17/05 11:27:14 AM

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:37:49 ; Search time 16.5753 Seconds
(without alignments)
638.529 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGSPVFLPPPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 44790

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	47.7	88	2 A30503	Ig gamma-2b chain
2	140	24.0	107	2 I68730	IgE chain C3 regio
3	139	23.8	107	2 I68726	IgE chain C3 regio
4	133	22.8	106	1 K3HU	Ig kappa chain C r
5	132	22.6	110	2 S43147	Ig upeilon chain -
6	128.5	22.0	105	2 B26434	Ig lambda-5 chain
7	128	22.0	99	2 S26653	Ig kappa chain C r
8	128	22.0	103	2 B26167	Ig lambda chain C
9	127.5	21.9	105	2 B30554	Ig lambda chain C
10	122.5	21.0	106	2 S00259	Ig lambda-5 chain
11	120.5	20.7	105	1 L1MS	Ig lambda-1 chain
12	120.5	20.7	106	2 S22760	Ig lambda-2 chain
13	118	20.2	104	2 F53275	Ig kappa-1 chain C
14	117	20.1	99	2 A37927	Ig kappa chain C r
15	116	19.9	102	2 B34509	Ig light chain C r
16	114	19.6	103	1 K4RB	Ig kappa-B4 chain
17	109.5	18.8	105	1 L2HU	Ig lambda chain C
18	109.5	18.8	105	2 H32529	Ig lambda chain C
19	108.5	18.6	98	2 S26654	Ig lambda chain C
20	107	18.4	106	2 I50740	Ig lambda chain C
21	106	18.2	104	1 K5RBV	Ig kappa chain C r
22	106	18.2	106	2 I50741	Ig lambda chain -
23	105.5	18.1	109	1 L7RB	Ig lambda chain C
24	100	17.2	105	2 A27390	Ig lambda chain C
25	99.5	17.1	105	1 L1PG	Ig lambda chain C
26	99.5	17.1	106	1 K4RBS	Ig kappa-2 chain C
27	99.5	17.1	106	2 G20907	Ig kappa-B4 chain
28	99	17.0	106	1 K1MS	Ig kappa chain C r
29	94	16.1	103	1 K5RB	Ig kappa-B5 chain

30 94 16.1 105 2 B27390 Ig lambda-2 chain
31 92.5 15.9 102 2 I46731 lambda-chain C-reg
32 92.5 15.9 104 1 K9RB Ig kappa-B9 chain
33 91 15.6 106 1 L1RTB Ig kappa chain C r
34 90 15.4 104 1 L3MS Ig lambda-3 chain
35 90 15.4 105 2 S22762 Ig lambda-2 chain
36 86 14.8 97 2 S26652 Ig gamma-1 chain C
37 86 14.8 106 1 K1RTA Ig kappa chain C r
38 84.5 14.5 78 2 C34509 Ig light chain C r
39 80.5 13.8 78 2 D34509 Ig light chain C r
40 79 13.6 82 2 I57802 Ig lambda2-like ch
41 79 13.6 90 2 A24629 Ig gamma-3 chain C
42 76.5 13.1 67 2 PLO186 Ig lambda chain, C
43 76 13.0 104 1 L2MS Ig lambda-2 chain
44 76 13.0 105 2 S22759 Ig lambda-2 chain
45 64.5 11.1 107 2 I68725 IGE chain C2 regio

ALIGNMENTS

RESULT 1

A30503

Ig gamma-2b chain C region (E5.7A12) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C/Accession: A30503

R/Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.

J. Immunol. 141, 1754-1761, 1988

A/Title: DNA rearrangements affecting both variable and constant regions of Ig H chain g

A/Reference number: A30503; MUID:88315788; PMID:2842402

A/Accession: A30503

A/Molecule type: mRNA

A/Residues: 1-88 <GIL>

A/Cross-references: GB:M21925

A/Experimental source: myeloma cell line MPC11

A/Note: the authors translated the codon GAG for residue 41 as Ser

C/Genetics:

A/Introns: 46/3

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F:1-70/Domain: immunoglobulin homology <IMM>

Query Match 47.7%; Score 278; DB 2; Length 88;

Best Local Similarity 63.2%; Pred. No. 6.6e-21;

Matches 48; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 24 SRTPEVTCVVVDYSDPEYQFNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDW 83

DB 1 SLTPKVTCCVVVDVSDDDPDVQISWVNNVEVHTAQQTQTHREDYNSTIRVSVSTLPIQHODW 60

QY 84 LNGKEYKCKVSNKGLP 99

DB 61 MSCKEPKCKVNNKDL 76

RESULT 2

I68730

IGE chain C3 region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C/Accession: I68730

R/Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A/Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s

A/Reference number: I54443; MUID:88152907; PMID:3346043

A/Accession: I68730

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-107 <RES>

A/Cross-references: GB:M222933; NID:G194464; PIDN:AAA37915.1; PID:G194469

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMM>

```
Query Match      24.0%; Score 140; DB 2; Length 107;
Best Local Similarity 30.7%; Pred. No. 5.3e-07;
Matches 35; Conservative 22; Mismatches 31; Indels 26; Gaps 5;

Qy 7 GPSVFLPPPKPKDTLMSRPTVTCVVVDV-SQBDPEVQFN-----MYVDGVEV 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 GVITYLIPPSPLD-LYQNGAPKLTCLVLDLSEKKNVNTWQEKKTVSASQWY---TKH 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 55 HNAKTKPREQFNSTYRVSVTLVTHQDLWLNKGYCKVSNKGLPSSIEKTIISK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 HN-----NATTSITSLPVAKDWIEGYGQICVDHPDPKPIVRSITK 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
I68726
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C:Accession: I68726
R:Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1998
A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s
A:Reference number: I54443; MUID:88152907; PMID:3346043
A:Accession: I68726
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:22-90/Domain: immunoglobulin homology <IMM>

Query Match      23.8%; Score 139; DB 2; Length 107;
Best Local Similarity 31.4%; Pred. No. 6.7e-07;
Matches 32; Conservative 20; Mismatches 48; Indels 2; Gaps 2;

Qy 7 GPSVFLPPPKPKDTLMSRPTVTCVVVDVVSQBDPEVQFNMYVDGVEVHNNAKTKPREEQF 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 GVITYLIPPSPLD-LYQNGAPKLTCLVLDLSE-KNVNTWQEKKTVPVSASQWYTKHHH 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 67 NSYRVSVSVTLVTHQDLWLNKGYCKVSNKGLPSSIEKTIISK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 NATTSITSLPVVAKDWIEGYGQICVDHPDPKPIVRSITK 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
K3HU
I9 kappa chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelmann, G.M.
Biochemistry 9, 3155-3161, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc
A:Reference number: A90562; MUID:71064023; PMID:5489770
A:Contents: myeloma protein Eu
A:Accession: B90562
A:Molecule type: protein
A:Residues: 1-106 <GOT>
A:Cross-references: UNIPROT:P01834
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
R:Gall, W.E.; Edelmann, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; Eu, disulfide bonds
R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A:Reference number: A91651; MUID:72188439; PMID:5027703
A:Contents: Bence Jones protein ri
A:Accession: A91651
A:Molecule type: protein
```

```
A:Residues: 1-106 <SUT>
R:Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
A:Reference number: A90806; MUID:81042304; PMID:6775818
A:Accession: A90806
A:Molecule type: DNA
A:Residues: 1-106 <HIE>
A:Cross-references: GB:J00241; NID:g331140; PIDN:CAA23823.1; PID:g1335148
A:Note: the sequence was determined from the germline gene
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, I
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, I
A:Reference number: A94417
A:Contents: Bence Jones protein Roy
A:Accession: A94417
A:Molecule type: protein
A:Residues: 1-44, A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>
A:Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R:Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A:Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A:Reference number: A91639; MUID:68242259; PMID:5586923
A:Contents: Bence Jones protein Cum
A:Accession: A91639
A:Molecule type: protein
A:Residues: 1-56, 'Q', 58-106 <HI2>
R:Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete i
A:Reference number: A92047; MUID:69234734; PMID:4893682
A:Contents: Bence Jones protein Ag
A:Accession: A92047
A:Molecule type: protein
A:Residues: 1-13, 'N', 15-106 <TIT>
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.
A:Reference number: A94242; MUID:70201507; PMID:5447531
A:Contents: Waldenstrom's macroglobulin Ou
A:Accession: A94242
A:Molecule type: protein
A:Residues: 1-13, 'N', 15-106 <KOH>
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A:Title: Km typing with PCR: application to population screening.
A:Reference number: A37927; MUID:91150772; PMID:1900145
A:Accession: B37927
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 8-106 <KUR>
A:Note: allotype Inv(3)
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances thei
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Genetics:
A:Gene: GDB:IGKC
A:Cross-references: GDB:120088; OMIM:147200
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapi
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>
F:26-86/Disulfide bonds: #status experimental
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match      22.8%; Score 133; DB 1; Length 106;
Best Local Similarity 30.5%; Pred. No. 2.6e-06;
Matches 32; Conservative 26; Mismatches 41; Indels 6; Gaps 3;

Qy 8 PSVFLPPPKPKDTLMSRPTVTCVVVDVVSQBDPEVQFNWYVDGV--EVHNAKTKPREEQ 65
```

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Db 5 PSVFIFPP--PSDEQLKSGTASVCLNNFYPREAKVQ--WKVDNALQSGNSQESVTEQDS 60
Qy 66 FNSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 61 KDSYVLSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 105

RESULT 5
S43147
Ig upsilon chain - duck (fragment)
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C:Accession: S43147
R:Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
submitted to the EMBL Data Library, March 1994
A:Description: Evidence from duck immunoglobulin genes that Igy is the common ancestor
A:Reference number: S43145
A:Accession: S43147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <MAG>
A:Cross-references: EMBL:X78355; NID:G468612; PID:G468613
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 22.6%; Score 132; DB 2; Length 110;
Best Local Similarity 30.3%; Pred. No. 3.5e-06;
Matches 30; Conservative 20; Mismatches 47; Indels 2; Gaps 2;

Qy 10 VFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTKPREEQNST 69
Db 12 IFVFPSP-GLYIRQDAKHCLVNL-PSDASISWTRKSGALRPDPMLTFHFNGT 69
Qy 70 YRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSK 108
Db 70 FTASSLSAISQDWLAGERFCTVQHEDLPFLGKSIK 108

RESULT 6
B26434
Ig lambda-5 chain C region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C:Accession: B26434
R:Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A:Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lympho
A:Reference number: A26434; MUID:87065143; PMID:3024017
A:Accession: B26434
A:Molecule type: mRNA
A:Residues: 1-105 <SAK>
A:Cross-references: GB:M30387
A:Note: the authors translated the codon TAC for residue 84 as Thr
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.0%; Score 128.5; DB 2; Length 105;
Best Local Similarity 34.3%; Pred. No. 7.3e-06;
Matches 36; Conservative 24; Mismatches 36; Indels 9; Gaps 6;

Qy 8 PSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDP-EVQFNWYDGVV-HNAKTKPREEQ 65
Db 6 PLVTLFPLSLKN-LQPTR-PQLVCL---VSEFYPGTLVDWVDGVPVQTGVETTPSKQ 60
Qy 66 FNSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 61 TNNKIMVSSYLLISDQWMPHSRYSRCVTHG--NTEKSVSPAE 103

RESULT 7
S26653
Ig kappa chain C region - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
```

```
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S26653
R:Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A:Reference number: S26652; MUID:91355693; PMID:2129418
A:Accession: S26653
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-99 <EHR>
A:Cross-references: EMBL:X65287
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 22.0%; Score 128; DB 2; Length 99;
Best Local Similarity 32.3%; Pred. No. 7.7e-06;
Matches 32; Conservative 22; Mismatches 39; Indels 6; Gaps 3;

Qy 8 PSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGV--EVHNAKTKPREEQ 65
Db 5 PSVFIFPP--PSDEQLKSGTASVCLNNFYPREAKVQ--WKVDNALQSGNSQESVTEQDS 60
Qy 66 FNSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEK 104
Db 61 KDSYVLSLSTLTSKADYKHKVYACEVTHQGLSSPVTK 99

RESULT 8
B26167
Ig lambda chain C region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B26167
R:Parvari, R.; Ziv, E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
A:Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germi
A:Reference number: A26167; MUID:87218480; PMID:3107981
A:Accession: B26167
A:Molecule type: mRNA; DNA
A:Residues: 1-103 <PAR>
A:Cross-references: UNIPROT:P20763; GB:M33049
A:Note: 90-Asp was found in one cDNA clone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-87/Domain: immunoglobulin homology <IMM>

Query Match 22.0%; Score 128; DB 2; Length 103;
Best Local Similarity 30.3%; Pred. No. 8e-06;
Matches 33; Conservative 24; Mismatches 44; Indels 8; Gaps 5;

Qy 2 PPVAGGSPVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTKP 61
Db 2 PKVA--PTTLFPPS-KEELNEATKATLVCLINDFFPS--PVTVDWIDG-STRSGTTA 55
Qy 62 REQFNSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 56 PQRQNSQYMASSVLSASDSSSHETTCRVTHG--TSITKTKRSE 102

RESULT 9
B30554
Ig lambda chain C region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30554
R:Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A:Reference number: A30554; MUID:89093962; PMID:2492052
A:Accession: B30554
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
```


RESULT 13

F53275
Ig kappa-1 chain C region b95 allotype - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: F53275
R:Avadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; MUID:91372868; PMID:1909995
A:Accession: F53275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <A>
A>Note: sequence inconsistent with nucleotide translation
C:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56170)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-87/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 118; DB 2; Length 104;
Best Local Similarity 29.1%; Pred. No. 8.1e-05;
Matches 32; Conservative 26; Mismatches 38; Indels 14; Gaps 6;
QY 3 PVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE----VHNAK 58
DB 2 PVA--PTVLFPSPSPAE--LATGTATTCVCV---ANKYFPDVTVMKVDGTTQTGTIENSR 54
QY 59 TKPREQFNSTYRVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISK 108
DB 55 TPQNSD--DCTYNLSSTLTLSKDEYNHSHDEYICQVA-QGSGSPVQSF 101

RESULT 14

A37927
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
C:Accession: A37927
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A:Title: Km typing with PCR: application to population screening.
A:Reference number: A37927; MUID:91150772; PMID:1900145
A:Accession: A37927
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-99 <KUR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 20.1%; Score 117; DB 2; Length 99;
Best Local Similarity 28.4%; Pred. No. 9.6e-05;
Matches 29; Conservative 26; Mismatches 41; Indels 6; Gaps 3;
QY 11 FLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV--EVHNAKTKPREQFNS 68
DB 1 FIFP--PSDQLKSGTASVCLLNFFYPREKQV--WKVDNALQSGNSQESVTEQDSKDS 56
QY 69 TYRVSVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110
DB 57 TYSLSSTLTLSKADYKHKLYACEVTHQGLSSPVTKSFNRGE 98

RESULT 15

B34509
Ig light chain C region 3 - sandbar shark (fragment)
C:Species: Carcharhinus plumbeus (sandbar shark)
C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 17-Nov-2000
C:Accession: B34509
R:Schluter, S.F.; Hohman, V.S.; Edmondson, A.B.; Marchalonis, J.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989
A:Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark

A:Reference number: A34509; MUID:90099382; PMID:2513577
A:Accession: B34509
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <SCH>
A:Cross-references: GB:M29044; NID:g212941; PIDN:AAA49153.1; PID:g212942
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 19.9%; Score 116; DB 2; Length 102;
Best Local Similarity 31.5%; Pred. No. 0.00013;
Matches 29; Conservative 18; Mismatches 41; Indels 4; Gaps 3;
QY 8 PSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG--VEVHNAKTKPREQF 66
DB 13 PSVSLLPSP--DQITAKNTATLCLVSGFKPGAAEIE--WTVDGSRGNGVETSRVQOEA 69
QY 67 NSTYRVSVSVLTVLHODWLNKGKCKVSNKGL 98
DB 70 DNTFSVSVSVLTLSASDWNHSHLYSCLVYKHEAL 101

Search completed: November 17, 2005, 07:55:08
Job time : 17.5753 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.8539 Seconds
(without alignments)
723.518 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583

Sequence: 1 APPVAGPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	22.8	106	1	KAC_HUMAN
2	128	22.0	103	1	LAC_CHICK
3	122.5	21.0	105	1	LAC5_MUSSP
4	120.5	20.7	105	1	LAC1_MOUSE
5	119.5	20.5	105	1	LAC5_MOUSE
6	114	19.6	103	1	KAC4_RABIT
7	112.5	19.3	106	2	Q8TCU5
8	109.5	18.8	105	1	LAC_HUMAN
9	106	18.2	104	1	KAC6_RABIT
10	105.5	18.1	105	1	LAC_RABIT
11	100	17.2	104	1	LAC1_RAT
12	99.5	17.1	105	1	LAC_FIG
13	99.5	17.1	106	1	KACB_RABIT
14	99	17.0	106	1	KAC_MOUSE
15	94	16.1	103	1	KAC5_RABIT
16	94	16.1	104	1	LAC2_RAT
17	92.5	15.9	104	1	KAC9_RABIT
18	91	15.6	106	1	KACB_RAT
19	90	15.4	104	1	LAC3_MOUSE
20	86	14.8	106	1	KACA_RAT
21	76	13.0	104	1	LAC2_MOUSE
22	76	13.0	105	2	Q99JC1
23	71	12.2	107	2	Q8KVI0
24	71	12.2	107	2	Q6EZI5
25	62.5	10.7	74	2	P79659
26	62.5	10.7	74	2	P79659
27	62	10.6	79	1	SNSP_HUMAN
28	62	10.6	93	2	Q6LBV9
29	61.5	10.5	93	2	Q6LBW2
30	61	10.5	98	2	Q7XZF9
31	59	10.1	73	2	Q8FBY4

32	59	10.1	93	2	Q31158
33	58.5	10.0	93	2	O19471
34	58.5	10.0	93	2	O19472
35	58.5	10.0	93	2	Q6GVI4
36	58.5	10.0	93	2	Q9QUH8
37	58	9.9	90	1	ALB2_SULTO
38	58	9.9	91	2	Q9JKF1
39	58	9.9	110	2	Q66084
40	57.5	9.9	74	2	P79661
41	57.5	9.9	95	1	DAFT_TRYCR
42	57	9.8	91	2	Q31248
43	57	9.8	106	2	Q31261
44	56.5	9.7	104	2	Q30837
45	56	9.6	63	2	Q6EHZ1

ALIGNMENTS

RESULT 1

KAC_HUMAN	ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Ig kappa chain C region.				
GN	Name=IGKC;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE (MYELOMA PROTEIN EU)				
RX	MEDLINE=71064023; PubMed=5489770;				
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."				
RL	Biochemistry 9:3155-3161(1970).				
RN	[2]				
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."				
RL	Biochemistry 9:3188-3196(1970).				
RN	[3]				
RP	SEQUENCE (BENCE-JONES PROTEIN TI).				
RX	MEDLINE=72188439; PubMed=5027703;				
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;				
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;				
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;				
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."				
RL	Cell 22:197-207(1980).				
RN	[5]				
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).				
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,				
RT	Steinmetz-Kayne M., Suter L., Watanabe S.;				
RL	(in) Franek F., Shugar D. (eds.);				
RL	Gamma Globulins: structure and function, pp.57-74, Academic Press, New York (1969).				
RN	[6]				
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).				
RX	MEDLINE=68242259; PubMed=5586923;				
RA	Hilschmann N.;				

Query Match					
Best Local Similarity 22.0%; Score 128; DB 1; Length 103;					
Matches 33; Conservative 24; Mismatches 44; Indels 8; Gaps 5;					
QY	2	PPVAGSPSVLFPKPKDILMISRTPEVTCCVVVDVSQEDPEVQFNWYVDGVVEHNAKTGP 61	: : : : :		
DB	2	PKVA--FTITLFPSPS-KEELNEATKVLVCILNDIFYS--PVTVDWIWG-STRSGETTA 55	: : : : :		
QY	62	RSEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGSLPSSIEKTISKAK 110	: : : : : :		
DB	56	PQRQSNQOYMASSYLSLASDWSSHETVTKRVTGNG--TSITKTLKESE 102	: : : : : :		
RESULT 3					
LACS MUSSP		STANDARD;		PRT;	105 AA.
ID	AC	P20765;			
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	IG	lambda-5 chain C region.			
OS	Mus spretus	(Western wild mouse).			
OC	Eukaryota;	Metazoa;			
OC	Mammalia;	Eutheria;			
OX	NCBI_TaxID=10096;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88196070;	PubMed=3129289;			
RA	Mami P., Cazenave P.A., Kindt T.J.;				
RT	"Conservation of the immunoglobulin C lambda 5 gene in the Mus genus."				
RL	EMBO J. 7:117-122(1988).				
CC	-/- SIMILARITY:	Contains 1 immunoglobulin-like domain.			
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation at				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/annouce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M35582; AAA39152.1; --				
DR	HSSP; P01843; LJNH.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig-cl.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00407; IGcl; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
DR	PROSITE; PS00290; IG_MHC; 1.				
KW	Immunoglobulin C region; Immunoglobulin domain.				
FT	NON TER	1			
FT	DOMAIN	6			
FT	DIVISUPID	27			
FT	DISULFID	104			
FT	SEQUENCE	105 AA; 11674 MW; AAB417DF68471A17 CRC64;			
SQ					
Query Match					
Best Local Similarity 21.0%; Score 122.5; DB 1; Length 105;					
Matches 35; Conservative 23; Mismatches 38; Indels 9; Gaps 5;					
QY	8	PSVFLPPKPKDILMISRTPEVTCCVVVDVSQEDP-EVQFNWYVDGVV-HNAKTPREEQ 65	: : : : :		
DB	6	PLVTLFLPFSLKNL----QANKVTLVLCI-VSEFYPGTLVDMVKDVGVPVGTQTQPSKQ 60	: : : : :		
QY	66	FNSTYRVSVSVLTVLHQDLNGKEYCKVSNKGSLPSSIEKTISKAK 110	: : : : : :		
DB	61	TNNKYMVSSYLTLLSDQMHPHSRYSCRVTHEG--NTVEKSVSPAEE 103	: : : : : :		
RESULT 4					
LACI MOUSE					

```
FT STRAND 10 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 52 54
FT STRAND 58 60
FT TURN 61 63
FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; 11575 MW; A89F2B09BCFCA018 CRC64;

Query Match 20.7%; Score 120.5; DB 1; Length 105;
Best Local Similarity 30.1%; Pred. No. 0.0003;
Matches 31; Conservative 21; Mismatches 44; Indels 7; Gaps 4;

QY 8 PSVFLPPPKDILMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV-HNAKTKPREQF 66
Db 6 PSVTLFPPSSEE--LETNKATLVCTITDF--YFGVWTVDMKVDGTPVTQGMETTPSQS 61

QY 67 NSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKSKA 109
Db 62 NNKYMASSYLTLTARAWERHSSVCQWTHGEG--HTVEKSLSRA 102

RESULT 5
LACS MOUSE
ID _LACS_MOUSE STANDARD; PRT; 105 AA.
AC P20784;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-5 chain C region.
GN Name=Igl-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065143; PubMed=3024017;
RA Sakaguchi N., Melchers F.;
RT "Lambda 5, a new light-chain-related locus selectively expressed in pre-B lymphocytes."
RL Nature 324:579-582(1986).
CC -!- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
CC EMBL; M30387; ; NOT_ANNOTATED_CDS.
CC HSSP; P01843; 1JNH.
CC MGD; MGI:96529; Igl-5.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC SMART; SM00407; Igc1_1.
CC PROSITE; PSS0835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
```

```
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11678 MW; 1F210915904A86A5 CRC64;

Query Match 20.5%; Score 119.5; DB 1; Length 105;
Best Local Similarity 33.3%; Pred. No. 0.00037;
Matches 35; Conservative 24; Mismatches 37; Indels 9; Gaps 6;

QY 8 PSVFLPPPKDILMISRTPEVTCVVVDVSQEDP-EVQFNWYVDGVEV-HNAKTKPREQ 65
Db 6 PLVTLEFLPSLKN-LQPTR-PQLVCL---VSEFYPTGLVDMKVDGVPVQTQVETTPSQ 60

QY 66 FNSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKSKA 110
Db 61 TNKNYVSSYLTLISDQWMPHSRTSCRVTHEG--NTVEKSVSPAE 103

RESULT 6
KAC4 RABIT
ID _KAC4_RABIT STANDARD; PRT; 103 AA.
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6412231;
RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4 alleleotype J-C locus and evidence for several b4-related sequences in the rabbit genome."
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit."
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S., Kindt T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody to streptococcal carbohydrate. II. Sequence determination of peptides from tryptic and peptic digests."
RL J. Biol. Chem. 250:3289-3296(1975).
CC -!- MISCELLANEOUS: This chain was obtained from antibody to the specific carbohydrate of group C Streptococci and was isolated from the serum of a single rabbit.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
CC EMBL; X00231; CAA25051.1; -.
CC PIR; A93971; K4RB.
CC HSSP; P01837; 1KCV.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Igi_1.
CC PROSITE; PSS0835; IG_LIKE; 1.
```

```
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 95 Ig-like.
FT DISULFID 26 85
FT DISULFID 103 103 Interchain (with a heavy chain).
FT CONFLICT 58 58 N -> D (in Ref. 3).
SQ SEQUENCE 103 AA; 11043 MW; 5FC5ACCB8B6B8DB CRC64;

Query Match 19.6%; Score 114; DB 1; Length 103;
Best Local Similarity 31.4%; Pred. No. 0.0013;
Matches 33; Conservative 20; Mismatches 38; Indels 14; Gaps 6;

QY 3 PVAGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE-----VHNAK 58
Dd 2 PVA--PTVLIPPAADQ--VATGRTIVCV---ANKYFPDVTVTWEVDGTTQTGTGIESK 54
QY 59 TKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE 103
Dd 55 TP--QNSADCTYNLSSTLTSTQYNSHKYETCKVT-QGTTSVVQ 96

RESULT 7
Q8TCJ5
ID Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp667J0810 (Fragment).
GN Name=DKFZp667J0810;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR HSSP; P01842; 1LIL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 19.3%; Score 112.5; DB 2; Length 106;
Best Local Similarity 28.7%; Pred. No. 0.0019;
Matches 29; Conservative 22; Mismatches 43; Indels 7; Gaps 4;

QY 8 PSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEYH-NAKTKPREQF 66
Dd 7 PSVTLFPPSSEE--LQANKATLVCLISDF--YPGAVTVAMKADSSPVKAGVETTTSPKQS 62
QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTIS 107
Dd 63 NNKYAASSYLSLTPEQWQKSHSKSCQVTHEG--STVEKTV 101

RESULT 8
LAC_HUMAN
ID LAC_HUMAN STANDARD; PRT; 105 AA.
AC P01842; P80423;

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
IG lambda chain C regions.
GN Name=IGLC1;
GN and
GN Name=IGLC2;
GN and
GN Name=IGLC3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE (BENCE-JONES PROTEIN SH).
MEDLINE=70156723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein. 3. The
complete amino acid sequence and the location of the disulfide
bridges.";
J. Biol. Chem. 245:2171-2176(1970).

[2]
SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
MEDLINE=69088380; PubMed=4883841;
Milstein C., Clegg J.B., Jarvis J.M.;
"Immunoglobulin lambda-chains. The complete amino acid sequence of a
Bence-Jones protein.";
Biochem. J. 110:631-652(1968).

[3]
SEQUENCE (BENCE-JONES PROTEIN NIG-64).
MEDLINE=83186114; PubMed=6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
"Comparative studies on the structure of the light chains of human
immunoglobulins. IV. Assignment of a subgroup.";
J. Biochem. 93:421-429(1983).

[4]
SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDLINE=71150336; PubMed=5549568;
Ponstingl H., Hees M., Hilschmann N.;
"Structural rule of antibodies. Primary structure of a monoclonal
immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
protein Kern). V. The complete amino acid sequence and its genetic
interpretation.";
Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).

[5]
PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
MEDLINE=74109253; PubMed=4814727;
Chen B.L., Poljak R.J.;
"Amino acid sequence of the (lambda) light chain of a human myeloma
immunoglobulin (IG New).";
Biochemistry 13:1295-1302(1974).

[6]
SEQUENCE (DOT).
MEDLINE=95252528; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
"Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).

[7]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
MEDLINE=75046825; PubMed=4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
Saul P.;
"The three-dimensional structure of the fab' fragment of a human
myeloma immunoglobulin at 2.0-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).

[8]
PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
MEDLINE=75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
"Primary structure of the MCG lambda chain.";
Biochemistry 13:4102-4114(1974).
```

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[9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RA Edmondson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
RL immunoglobulin light chains.";
[10]
RP Biochemistry 14:3953-3961(1975).
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG.
RA MEDLINE=90131913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmondson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms.";
RL J. Mol. Biol. 210:601-615(1989).
[11]
RP SEQUENCE FROM N.A.
RP MEDLINE=82080680; PubMed=6273747;
RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT "Clustered arrangement of immunoglobulin lambda constant region genes
RT in man.";
RL Nature 294:536-540(1981).
CC -!- MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain
CC found in proteins SH, X, and NIG-64. The Kern protein has the
CC Kern+ marker, the NEW protein has the Oz+ marker, the Mcg protein
CC has the Kern+ marker, and the Mcg+ marker.
CC -!- MISCELLANEOUS: Six tandem lambda-type genes were identified and
CC the 3 most 5' were sequenced. These correspond to the Mcg sequence
CC (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+
CC sequence (lambda-3).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
DR EMBL; J00253; AAA59107.1; -
DR EMBL; L38562; AAB36581.1; ALT_INIT.
DR EMBL; X51754; CAB38569.1; ALT_INIT.
DR EMBL; X51755; CAA36049.1; -.
DR EMBL; X51755; CAA36051.1; -.
DR PIR; A92057; L2HU.
DR PDB; 1AOK; X-ray; L=1-105.
DR PDB; 1LIL; X-ray; A/B=1-105.
DR PDB; 2MCG; X-ray; -.
DR PDB; 7FAB; X-ray; L=1-105.
DR Genew; HGNC:5855; IGLC1.
DR Genew; HGNC:5856; IGLC2.
DR Genew; HGNC:5857; IGLC3.
DR H-INVDB; HIX0016285; -.
DR MIM; 147220; -.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Fram; PFO0047; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00230; IG_MHC; 1.
KW 3d-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT VARIANT 104 104 Interchain (with heavy chain).
FT VARIANT 5 5 A -> N (in MCG+ marker).
FT VARIANT 7 7 S -> T (in MCG+ marker).
FT VARIANT 45 45 S -> G (in Kern+ marker).
FT VARIANT 45 45 S -> G (in Kern+ marker).
FT /FTId=VAR_003900.

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FT VARIANT 56 56 T -> K (in MCG+ marker).
FT /FTId=VAR_003901.
FT VARIANT 82 82 R -> K (in Oz+ marker).
FT /FTId=VAR_003902.
FT STRAND 8 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 24 32
FT STRAND 38 43
FT TURN 44 45
FT STRAND 46 48
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 72
FT HELIX 75 80
FT STRAND 84 89
FT STRAND 94 99
SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;
Query Match 18.8%; Score 109.5; DB 1; Length 105;
Best Local Similarity 27.7%; Pred. No. 0.0037;
Matches 28; Conservative 23; Mismatches 43; Indels 7; Gaps 4;
QY 8 PSVFLPPPKDILMSRTPETVCVVVDSQEDPEVQFNWYVDGVEVH-NAKTKPREEQF 66
Db 6 PSVTLFPPSSEE--LQANKATLVCLISDF--YPGAVTVAKADSSPVKAGVETTPSKQS 61
QY 67 NSTYRVSVLVTLVHQDLNGKEYKCKVSNKGJLPSSLEKTIIS 107
Db 62 NNKYAASSYLSLTPEQWKSRRSYSCQVTHEG--STVEKTVA 100
RESULT 9
KAC6_RABIT STANDARD; PRT; 104 AA.
AC P03984;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Ig kappa chain b5 variant C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (CLONE PKB5-P2).
RX MEDLINE=64041515; PubMed=6314281;
RA Bernstein K.E., Skuria R.M. Jr., Mage R.G.;
RT "The sequences of rabbit kappa light chains of b4 and b5 allotypes
RT differ more in their constant regions than in their 3' untranslated
RT regions.";
RL Nucleic Acids Res. 11:7205-7214(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=6424123;
RA Emorine L., Sogon J.A., Trinh D., Kindt T.J., Max E.E.;
RT "A genomic gene encoding the b5 rabbit immunoglobulin kappa constant
RT region: implications for latent allotype phenomenon.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1789-1793(1984).
CC -!- MISCELLANEOUS: The cDNA from which this sequence was derived
CC contains a terminator codon within the V-region coding region. The
CC origin of this codon and of the differences between this and other
CC sequenced b5 C regions are unclear. The cDNA clone was made using
CC mRNA from trypanosome-infected b5-homozygous rabbits.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----NOT_ANNOTATED_CDS.
CC ENBL; X00032; -, NOT_ANNOTATED_CDS.
DR ENBL; K01363; AAA31355.1; -.
DR PIR; A02124; KSRBV.
DR HSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 100 Ig-like.
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
FT CONFLICT 1
FT CONFLICT 1 A -> VA (in Ref. 2)
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match
Best Local Similarity 18.2%; Score 106; DB 1; Length 104;
Matches 28; Conservative 25; Mismatches 40; Indels 12; Gaps 5;

QY 8 PSVFLPPPKKDTLMISRTVEVTCVVVDVSDQEDPEVFQFNWYVDG-----VEVHNATKPRE 63
DB 5 PTVLFFPPSPAE--LATGTATVVCV---ANKYFPDGTVTWQVDGKPLTTGTIETSKTPQNS 59
QY 64 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 60 D--DCTNLSTLTKSDEYNHDEYTCQVA-QGSGSPVQVSFSR 101

RESULT 10
LAC_RABIT
ID LAC_RABIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=82091105; PubMed=6797414;
RA Garcia I., Jaton J.-C.;
RT "The primary structure of the constant region of Basilea-rabbit
immunoglobulin lambda-chains.";
RL Biochem. J. 197;177-183(1981).
CC -1- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
specificity.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02130; L7RB.
DR HSP; P01842; 1AQA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11484 MW; B42751327286663D CRC64;

Query Match
18.1%; Score 105.5; DB 1; Length 105;

us-09-674-857-12.LL.rup
Best Local Similarity 26.9%; Pred. No. 0.0093;
Matches 28; Conservative 22; Mismatches 47; Indels 7; Gaps 4;

QY 8 PSVFLPPPKKDTLMISRTVEVTCVVVDVSDQEDPEVFQFNWYVDGVEV-HNAKTKPREQF 66
DB 6 PSVILFPSPSEE--LKDKNKATLVCLISDFYPR--TVKVNWKADGNSVTQGVDTTQPSKQS 61
QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 62 NNKYAASSFLHLTANQWKSQSVTCQVTHEG--HTVEKSLAPAE 103

RESULT 11
LAC1_RAT
ID LAC1_RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
and a single V lambda gene.";
RL Gene 55;75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR ENBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01843; LUNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC878A CRC64;

Query Match
17.2%; Score 100; DB 1; Length 104;
Best Local Similarity 27.4%; Pred. No. 0.033;
Matches 29; Conservative 22; Mismatches 43; Indels 12; Gaps 5;

QY 8 PSVFLPPPKKDTLMISRTVEVTCVVVDVSDQEDPEVQ-FNMYVDGVEVHNATKPREE 64
DB 6 PSVTLFPSPSEEL---KTDKATLVCMVTDYF---PGVMVVMWKADGTPITQGVETTQPF 58
QY 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 59 KQNNKYMATSYLLLTAKAWETHSNYSQVTHE--ENTVEKSLRAE 102

RESULT 12
LAC_PIG
ID LAC_PIG STANDARD; PRT; 105 AA.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.6073 Seconds
(without alignments)
347.833 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGPSVFLPPPKPKDT.....CKVSNKGLPSSIBKTIKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUTS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	565	96.9	110	3	US-08-444-644-44
2	565	96.9	110	3	US-08-232-246A-44
3	561	96.2	109	2	US-08-070-116A-4
4	561	96.2	109	4	US-08-557-050-4
5	542.5	93.1	109	3	US-08-444-644-30
6	542.5	93.1	109	3	US-08-232-246A-30
7	541	92.8	110	3	US-08-444-644-21
8	541	92.8	110	3	US-08-232-246A-21
9	525	90.1	105	2	US-08-232-539D-60
10	525	90.1	110	3	US-08-444-644-38
11	525	90.1	110	3	US-08-232-246A-38
12	328	56.3	66	3	US-08-569-147-85
13	179	30.7	107	4	US-09-281-760B-36
14	166.5	28.6	106	2	US-08-232-539D-54
15	152	26.1	109	3	US-08-466-163B-1
16	152	26.1	109	4	US-09-802-096-1
17	152	26.1	109	4	US-09-802-077-1
18	142	24.4	100	1	US-08-422-101-10
19	142	24.4	100	1	US-08-422-091-10
20	142	24.4	100	2	US-08-422-092-10
21	142	24.4	100	2	US-08-788-800-7
22	142	24.4	100	3	US-08-422-093-10
23	142	24.4	100	3	US-08-422-112-10
24	133	22.8	105	3	US-09-025-769B-166
25	133	22.8	105	4	US-09-490-070A-166
26	133	22.8	105	4	US-09-490-153-166
27	133	22.8	105	4	US-09-490-324-166

28 133 22.8 106 2 US-08-378-939-40 Sequence 40, Appl
29 133 22.8 106 2 US-08-761-277A-49 Sequence 49, Appl
30 133 22.8 106 3 US-08-444-644-26 Sequence 26, Appl
31 133 22.8 106 3 US-08-232-246A-26 Sequence 26, Appl
32 133 22.8 107 1 US-08-422-101-8 Sequence 8, Appl
33 133 22.8 107 1 US-08-422-091-8 Sequence 8, Appl
34 133 22.8 107 2 US-08-422-092-8 Sequence 8, Appl
35 133 22.8 107 2 US-08-788-800-5 Sequence 5, Appl
36 133 22.8 107 3 US-08-422-093-8 Sequence 8, Appl
37 133 22.8 107 3 US-08-422-112-8 Sequence 20, Appl
38 133 22.8 107 4 US-09-301-593-20 Sequence 13, Appl
39 133 22.8 108 4 US-09-313-942-13 Sequence 7, Appl
40 129 22.1 106 1 US-08-399-106A-7 Sequence 7, Appl
41 129 22.1 106 1 US-08-433-105A-7 Sequence 7, Appl
42 129 22.1 106 2 US-08-434-869A-7 Sequence 7, Appl
43 127.5 21.9 109 2 US-08-646-981-6 Sequence 6, Appl
44 127 21.8 109 1 US-08-436-463-8 Sequence 8, Appl
45 127 21.8 109 1 US-08-024-253-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Fiden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
FILING DATE: 07-JUL-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-8240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-44

Query Match          96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 2
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Fiden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-44

Query Match          96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-070-116A-4

Query Match          96.2%; Score 561; DB 2; Length 109;
Best Local Similarity 97.2%; Pred. No. 4e-60;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61
Db 1 PEFLGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 3
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: Of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-070-116A-4

Query Match          96.2%; Score 561; DB 2; Length 109;
Best Local Similarity 97.2%; Pred. No. 4e-60;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61
Db 1 PEFLGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 4
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
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; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Willson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match 96.2%; Score 561; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 4e-60; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 3;

Qy 2 PVVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKP 61
Db 1 PEFILGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKP 60

Qy 62 REQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 REQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 5
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match 93.1%; Score 542.5; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-58;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 59

Qy 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 60 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTIKTK 109

RESULT 6
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-30

Query Match 93.1%; Score 542.5; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-58;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 59

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
Db 60 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKTK 109

RESULT 7
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-21

Query Match 92.8%; Score 541; DB 3; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.1e-57;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 1 APPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVYKFNYDGVGVHNAKTK 60

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110

RESULT 8
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
```



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TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match          92.8%; Score 541; DB 3; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.1e-57;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYDGVVHNAKTK 60
Db 1 APELLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSDHEDPEVFQFNWYDGVVHNAKTK 60

Qy 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
Db 61 PREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 9
US-08-232-539D-60
; Sequence 60, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IgE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-60

Query Match          90.1%; Score 525; DB 2; Length 105;
Best Local Similarity 94.2%; Pred. No. 8.6e-56;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 GPSVFLPPPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYDGVVHNAKTKPREEQF 66
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TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match          92.8%; Score 541; DB 3; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.1e-57;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYDGVVHNAKTK 60
Db 1 APELLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSDHEDPEVFQFNWYDGVVHNAKTK 60

Qy 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
Db 61 PREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 10
US-08-444-644-38
; Sequence 38, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-38

Query Match          90.1%; Score 525; DB 3; Length 110;
Best Local Similarity 90.0%; Pred. No. 9.2e-56;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSDQEDPEVFQFNWYDGVVHNAKTK 60
Db 1 APELLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSDHEDPEVFQFNWYDGVVHNAKTK 60

Qy 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
Db 61 LREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110
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RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/082322246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match 90.1%; Score 525; DB 3; Length 110;
Best Local Similarity 90.0%; Pred. No. 9.2e-56;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNKTK 60
Db 1 APELLGGPSVFLPPTPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNKTK 60

Qy 61 PREQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 LREEQNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPAPIETISKAK 110

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
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; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match 56.3%; Score 328; DB 3; Length 66;
Best Local Similarity 90.9%; Pred. No. 3.1e-32;
Matches 60; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDGLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNKTK 60
Db 1 APELLGGPSVFLPPTPKDGLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNKTK 60

Qy 61 PREEQF 66
Db 61 PREEQY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)-(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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Db 65 NGTLVTSTLPVGTROWIEG-ETQCRVTHPHLPALMRSTTK 105

Search completed: November 17, 2005, 07:53:56
Job time : 23.6073 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 83.1279 Seconds
(without alignments)
553.666 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGSPVFLPPPKPDKT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0
Maximum DB seq length: 110

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	98.8	110	18	US-10-959-318-9
2	573	98.3	110	18	US-10-959-318-10
3	571	97.9	110	20	US-11-018-102-25
4	565	96.9	110	18	US-10-959-318-4
5	565	96.9	110	18	US-11-018-102-24
6	562	96.4	110	18	US-10-959-318-13
7	562	96.4	110	18	US-10-959-318-21
8	561	96.2	109	14	US-10-267-286A-4
9	560	96.1	110	18	US-10-959-318-7
10	559.5	96.0	109	18	US-10-959-318-11
11	559	95.9	110	18	US-10-959-318-14
12	558	95.8	110	18	US-10-959-318-9
13	557	95.5	109	18	US-10-959-318-12
14	547.5	93.9	109	18	US-10-959-318-17
15	546	93.7	110	18	US-10-959-318-5
16	545.5	93.6	109	18	US-10-959-318-15
17	545	93.5	110	20	US-11-018-102-23
18	544.5	93.4	109	18	US-10-959-318-18
19	543	93.1	110	18	US-10-959-318-6
20	542.5	93.1	109	18	US-10-959-318-2
21	542.5	93.1	109	18	US-10-959-318-16
22	542	93.0	109	18	US-10-627-556-270
23	542	93.0	110	18	US-10-959-318-24
24	542	93.0	110	18	US-10-959-318-25
25	541	92.8	110	15	US-10-370-743-23
26	541	92.8	110	18	US-10-959-318-1
27	541	92.8	110	18	US-10-959-318-22
28	541	92.8	110	18	US-10-959-318-23
29	541	92.8	110	20	US-11-018-102-22
30	538	92.3	102	18	US-10-609-783B-57
31	538	92.3	102	18	US-10-609-783B-59
32	537	92.1	109	14	US-10-207-655-220
33	537	92.1	109	18	US-10-627-556-14
34	536	91.9	109	14	US-10-020-354-80
35	536	91.9	110	15	US-10-370-749-53
36	536	91.9	110	18	US-10-959-318-19
37	534	91.6	110	15	US-10-370-743-51
38	533	91.4	109	18	US-10-627-556-294
39	533	91.4	110	18	US-10-959-318-20
40	532	91.3	109	18	US-10-627-556-258
41	532	91.3	109	18	US-10-627-556-278
42	532	91.3	109	18	US-10-627-556-302
43	531	91.1	110	17	US-10-491-653-22
44	531	91.1	110	18	US-10-959-318-3
45	529	90.7	109	14	US-10-207-655-322

RESULT 1
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)
US-10-959-318-9

Query Match 98.8%; Score 576; DB 18; Length 110;
Best Local Similarity 98.2%; Pred. No. 3.9e-48;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 1 APPVAGSPVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60


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; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-13

Query Match          96.4%; Score 562; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 9e-47;
Matches 105; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNKYVGGVVEVHNATK 60
Db 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNKYVGGVVEVHNATK 60

Qy 61 PREEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKGLPAPIETISKAK 110

RESULT 7
US-10-959-318-21
; Sequence 21, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG4 CH2 sequence with delta e (E268) mutation
US-10-959-318-21

Query Match          96.4%; Score 562; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 9e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNKYVGGVVEVHNATK 60
Db 1 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNKYVGGVVEVHNATK 60

Qy 61 PREEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
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RESULT 8
US-10-267-286A-4
; Sequence 4, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:0040USCI
; CURRENT APPLICATION NUMBER: US/10/267,286A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-4

Query Match          96.2%; Score 561; DB 14; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-46;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNKYVGGVVEVHNATK 61
Db 1 PEFLLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNKYVGGVVEVHNATK 60

Qy 62 REEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 109

RESULT 9
US-10-959-318-7
; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
; OTHER INFORMATION: mutations
US-10-959-318-7

Query Match          96.1%; Score 560; DB 18; Length 110;
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/ OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-14

Query Match          95.5%; Score 559.5; DB 18; Length 109;
Best Local Similarity 97.3%; Pred. No. 1.5e-46;
Matches 105; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREEQNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-11

Query Match          96.0%; Score 559.5; DB 18; Length 109;
Best Local Similarity 97.3%; Pred. No. 1.5e-46;
Matches 107; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APPVA-GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 PREEQNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-14

Query Match          95.5%; Score 557; DB 18; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.7e-46;
Matches 104; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREEQNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-959-318-12
; Sequence 12, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 12
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-8

Query Match          95.5%; Score 557; DB 18; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.7e-46;
Matches 104; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREEQNSTYRVSVLTVTLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-959-318-8
; Sequence 8, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-8
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; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-12

Query Match 95.5%; Score 556.5; DB 18; Length 109;
Best Local Similarity 96.4%; Pred. No. 3e-46;
Matches 106; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
Qy 1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 59
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 110
Db 60 PREEQNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 109

RESULT 14
US-10-959-318-17
; Sequence 17, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta d (D268) mutation
US-10-959-318-17

Query Match 93.9%; Score 547.5; DB 18; Length 109;
Best Local Similarity 94.5%; Pred. No. 2.3e-45;
Matches 104; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Qy 1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 59
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 110
Db 60 PREEQNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPAPIEKTISKTK 109

RESULT 15
US-10-959-318-5
; Sequence 5, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07

; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta d (Q268) mutation
US-10-959-318-5
Query Match 93.7%; Score 546; DB 18; Length 110;
Best Local Similarity 92.7%; Pred. No. 3.2e-45;
Matches 102; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPELLGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 110
Db 61 PREEQNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPAPIEKTISKAK 110

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Job time : 84.1279 secs

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